

OM of: US-10-031-904-8 to: N\_Geneseq\_032802.\* out\_format: pfs  
 Date: Oct 9, 2002 6:42 PM  
 About: Results were produced by the GenCore software, version 4.5,  
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## Command line parameters:

-MODE=frame+model -DEV=xlh  
 -Q=/cgn2.1/USPPO\_Spool/US10031904/runat\_09102002\_084257.23681/app-query.fasta.1.232  
 -Db=N\_Geneseq\_032802 -QFWT=fastap -SUFFIX=p2n.rng -GAPOP=12.000  
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000  
 -GAPOP=6.000 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
 -FGAPOP=6.000 -FGAPEXT=7.000 -STAR=1 -MATRIX=blom62  
 -TRANS=human10.cdl -LIST=45 -DOCLIGN=200 -THR\_SCORE=pct  
 -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pts  
 -NORM\_ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
 -USER=US10031904 -CGN1\_1.481 -NCPU=6 -ICPU=3 -LONGLOG  
 -DEV\_TIMECUT=120 -WARN\_TIMECUT=30 -NO\_XLPHY -NAIT -THREADS=1

## Search information block:

Query: US-10-031-904-8  
 Query length: 174  
 Database: N\_Geneseq\_032802.\*  
 Database sequences: 176436  
 Database length: 859457221  
 Search time (sec): 175.470000

Sequence	Strd Orig	ZScore	E_Score	len	Documentation
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA564602 +		946.00	1870.05	8.2e-96	9
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AA564474 +		649.50	1253.09	1.9e-61	7
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:AA591477 +		649.50	1252.37	2.1e-61	69
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AAQ11642 +		649.50	1252.37	2.1e-61	69
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AA538150 +		649.50	1251.82	2.2e-61	7
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/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AA53269 +		635.00	1250.09	2.8e-61	59
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AA53270 +		635.00	1250.09	2.8e-61	59
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AA53271 +		635.00	1250.09	2.8e-61	59
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AA53272 +		635.00	1250.09	2.8e-61	59
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AA53273 +		635.00	1250.09	2.8e-61	59
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:AAQ41667 +		634.50	1222.44	9.6e-60	69
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AA564473 +		513.00	989.83	8.7e-47	2
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:AA564289 +		487.00	937.94	6.8e-44	2
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/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA501504 +		308.00	592.31	2.0e-24	9
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/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AA17599 +		289.00	551.59	2.2e-22	12
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:AAQ90306 +		289.00	549.74	2.8e-22	14
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:AAQ93106 +		289.00	549.36	3.0e-22	15
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:AAQ93339 +		289.00	549.36	3.0e-22	15
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AAQ10864 +		289.00	549.24	3.0e-22	15
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/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAQ20370 +		289.00	547.31	3.9e-22	1
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AA46065 +		289.00	547.14	4.0e-22	18
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AAQ14915 +		289.00	546.51	4.3e-22	19
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AA18370 +		289.00	541.04	8.7e-22	3
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AA117598 +		287.00	548.00	3.2e-22	11
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:AA17596 +		287.00	548.60	3.2e-22	11
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AAV08935 +		272.50	519.55	1.4e-20	11
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:AA587915 +		272.50	516.69	2.0e-20	14
/SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:AAAN70047 +		272.50	513.45	3.0e-20	20

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 /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:AA591044 + 272.50 512.34 3.4e-20

seq\_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA564602

## seq\_documentation\_block:

ID AAF58602 standard; cDNA: 627 BP.

AA564602;

24-APR-2001 (first entry)

Human RECAP polynucleotide, SEQ ID NO: 30.

Human; RECAP: receptors and associated proteins; cerebroprotective;

neurotrophic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV;

antidiabetic; immunostimulant; immunomodulator; antiinflammatory;

antithyroid; immunosuppressive; nephrotropic; antigout; thyromimetic;

cytostatic; antibacterial; virucide; fungicide; protozoacide;

antiartherosclerotic; hepatotropic; gene therapy; infection; cancer; ss.

Homo sapiens.

21-JUL-2000; 2000MO-US20035.

21-JUL-1999; 99US-0145232.

07-OCT-1999; 99US-0158578.

12-NOV-1999; 99US-0165192.

(INCY-) INCYTE GENOMICS INC.

An-Young J, Bandman O, Tang YT, Yue H, Azimzal Y, Burford N;

Baughn MR, Lu DM, Hillman JL, Patterson C, Lal P;

WPI: 2001-168554/17.

P-PSDB: AAB8878.

Claim 5: Page 120; 128pp: English.

The present sequence encodes a human RECAP (receptors and associated proteins) polypeptide. RECAP polynucleotides and polypeptides are useful in the diagnosis, treatment and prevention of neurological disorders such as stroke, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease, Down's syndrome, amyotrophic lateral sclerosis, multiple sclerosis, bacterial and viral meningitis, CJD (Creutzfeldt-Jakob disease), GSS (Gerstmann-Strausner-Scheinker syndrome), immunological disorders, including autoimmune/inflammatory disorders such as AIDS, Digeorge's syndrome, severe combined immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's disease, Addison's disease, autoimmune thyroiditis, Crohn's disease, diabetes mellitus, Good pasture's syndrome, gout, Grave's diseases, Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections; and cell proliferation disorders such as arteriosclerosis, atherosclerosis, cirrhosis, hepatitis and cancer.

Sequence 627 BP; 142 A; 173 C; 128 G; 184 T; 0 other:

alignment\_scores: Quality: 946.00 Length: 174

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Ratio: 5.437      Gaps: 0
Percent Similarity: 100.000  Percent Identity: 100.000
alignment block:
US-10-03T-904-8 x AAF58602  ..

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Align seg 1/1 to: AAF58602 from: 1 to: 627

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1 MetalIaProPovaAlArgLeuGIARProPhoPSeSerARqArpHeR 17
87 ANGGCGCTCCCGACCGCGTCTGAGCGACGTCCTTTCCTTCCGGCGCTTCC 136
17 OGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
137 TGGGTGCTCTCTGGGGCGCTGGGTGGTGGCGTCTCTCTCTCCGAGATC 186
34 IncYasNValProGIuTrPLeuProPheAlaArpProThrAsnLeuThr 50
187 AATGCAAATGTCGGGAATGGCTTCATTTTCCAGGCTCAACCACTAACT 236
51 AspApPheGIuPheProIleGIyThrTyrLeuAsnTyrGIuCyAsnArp 67
237 GATGACTTTGGATTTCCTCATTTGGACACTATCTGAAGCTATGAATGACGCGCC 286
67 OGlyTyrSerGIyArpProPheSerIleIleCyLeuLysAsnSerValT 84
287 TGGTATTTCCGGAAGACCGTTTCTATACATCTCTCAAAAACTCAGTCT 336
84 rPthSerAlaLysAspLysCysLysArqLysSerCysArqAsnProP 100
337 GGACAAGGCTAAGACAAAGTCAAAAGTAAATCATTGTAATCOTGCA 386
101 AsPProValAsnGIuMetAlaHisValIleLysAspIleGIuPheGIyS 117
387 GATCTTGGAATGGCATAGGCAACATGATGATAAAGACATCAGATGGGAGC 436
117 rGIaIleLysTyrSerCysProLysGIyTyrArgLeuIleGIySerSers 134
437 CCAAAATTAATATCTTGCTCTAAAGGATACCGACATCATTTGGTCTCGT 486
134 eRAlaThrCysIleIleSerGIyAsnThrValIleTrpAspAsnLysThr 150
487 CTGGCCACATGCATATCTCAGGCAACACGTCTCATTTGGGATATATAACA 536
151 ProValCyAspSerGIuLeuLysTyrAlaPheLeuPheLeuLeuProI 167
537 CCTGTTTGTGCACTGAGTTGAATAATGACATTCCTATTTCTTTTACCGAT 586
167 eHisSerAsnPheSerLeuGI 174
587 ACATCTCAATTTTCTCTGGAA 608
seq_name: /SIDS1/cgndata/geneseq/geneseq-emb1/NA2001B.DAT:ANS64474/

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AC	AAS64474 standard; cDNA; 7821 BP.
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XX	AAS64474;
DT	13-FEB-2002 (first entry)
XX	
DE	DNA encoding novel human diagnostic protein #278.
XX	
KM	Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss
XX	
OS	Homo sapiens.
PX	
PN	WO200175067-A2.
KX	
PD	11-OCT-2001.
XX	
XX	30-MAR-2001; 2001WO-US08631.
XF	

XX	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	(HYSEQ-) HYSEQ INC.
PA	
PI	Dmanac RT, Liu C, Tang YT;
PT	WPI; 2001-639362/73.
DR	P-PSDB; ABE00287.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
PS	Claim 1; SEQ ID No 278; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy technique
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
XX	Sequence 7821 BP; 1986 A; 1904 C; 1883 G; 2046 T; 2 other;

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alignment_scores:      Quality: 650.50      Length: 149
                       Ratio: 4.884      Gaps: 2
Percent Similarity:    89.933      Percent Identity: 81.208

alignment block:
US-10-031-904-8 x AAS64474 ..

Align seg 1/1 to: AAS64474 from: 1 to: 7821

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9  ArgProPheProSerAlaGlyPhe.....ProIlyLeuLeuLeuAlaI 23
   ::::: ::::: ::::: ::::: :::::
497 CACCGCGGCGCCGGTCCTCCCTTCGTCGCGAGAGAACCTCGTGGCGGT 546
   ::::: ::::: ::::: ::::: :::::
23  alaValLeuLeu...LeuSerSerSerAspGlnCysAlaValAlaPro 39
   ::::: ::::: ::::: ::::: :::::
547 CGTGGTGGTGGTCCGCGTCCGGGTGGCCGGGGGTCATGCAATGCCCGAG 596
   ::::: ::::: ::::: ::::: :::::
39  InIrrPheProPheAlaArgProThrAsnLeuThrAspPheGluPhe 55
   ::::: ::::: ::::: ::::: :::::
597 AATGGCTTCATTGGCCAGAGCCACCAACCTACTGATGAGTTGAGTTT 644
   ::::: ::::: ::::: ::::: :::::
56  ProIleGlyThrIleLeuAsnArgIleCysArgProGlyIlySerGlyAla 72
   ::::: ::::: ::::: ::::: :::::
647 CCAATTGGAGAAATATTCGAACTATGAAATGCGCCCTGATATCCGGAG 696
   ::::: ::::: ::::: ::::: :::::
72  gpProPheSerIleIleCysLeuIlyAsnSerValTrrPheSerAlaIysa 89
   ::::: ::::: ::::: ::::: :::::
697 ACCGTTTCTATCATCTCGCCCTAAAAACTCATGCTGGACGGGCTCAAGG 746
   ::::: ::::: ::::: ::::: :::::

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seq_documentation_block:
ID      AAN91477 standard; DNA; 6951 BP
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AC	AA091477;
XX	
DT	22-FEB-1990 (first entry)
XX	
DE	CRI protein DNA.
XX	
KW	Complement; cofactor.
XX	
OS	Homo sapiens (human).

uman).

FH	key	Location/Qualifiers
FH	0000+1430	38 147

28..147

ET 1 6951

FT                000  
                    4 : 0004  
                    /\*tag= b

FT	CDS	28..6147
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/notes="CBI protocol"

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FT	CDS	7 MOSES - CMT PROTEIN
FT		28. .1533

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ET / *tag= d
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/note="CRI protein"

W08909220-A.

1

PD 05-OCT-1989.  
XX

31-MAR-1989: 89WO-US01358.

XX

PR 01-APR-1988; 88US-0176532.  
PR

AA  
PA (TCEL-) T CELL SCIENCES INC.

PA (UYJO ) THE JOHNS HOPKINS UNIVERSITY

PA (BRIG ) THE BRIGHAM AND WOMENS HOSE  
PA  
XX

aa  
PI Fearon DT, Klickstein LB, Wong W.

XX

DR WPI; 1989-309498/42.

P-PSDB; AAF92219.  
DK  
XX

PT New nucleic acid sequences encoding

PT for diagnosis and control of complex

XX Inflammation, myocardial infarct, e

PS Claim 1; fig. 1; 191pp; English.

XX  
XX

CC This is full-length CRI protein, and  
CC the transmembrane region. The prote

C4b, have cofactor activity and inhibit

CC They are useful in diagnosing and t

CC pertusion injury.

Sequence 6951 BP; 1802 A; 1680 C; 1

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	Quality:	649.50	
	Ratio:	4.883	Gaps: 2
	Percent Similarity:	89.865	Percent Identity: 81.757
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	US-10-031-904-8 x AAN91477	..	
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XX	:::		:::
XX	70 CCGGCGCCCGTCCCTCCCCTGTGGTGCGAGGAGVCCCTTCGGCGGTTGT 119		
XX	24 uValleuLeu...LeuSerSerPheSerAspGlnCysAaenValProglut 40		
XX	:::		:::
XX	120 GNGTCCTCTTGGCCGCTCGGTGGCTCGGTGCATCAATGCCCCAGAT 169		
XX	40 rPlauProPheaIaaArgProthrAsnLeuthrAspAspPheGluPhePro 56		
XX	170 GGCTTCATTGGCAGGCGCTACCAACTACTACTGATGAGTTGAGTTGCC 219		
XX	57 lIleGlyThrTyrlEuasnlTYrGluCysArgProGlYTYrSerGIATyRPr 73		
XX	220 ATTGGGACAAATCTAACACTATGAATGCCGCCCTGgTtATTCGGAGAACC 269		
XX	73 oPhseSerllellecysLEuylsaenserValITppHsrerAlalysapl 90		
XX	:::		:::
XX	270 GTTTCATCATCTGCTTAATAAACTAGTCTGACTGCTGACTAGACA 319		
XX	90 yscysLysArglyssercysArqasnProBraapBrovalAsnGlywet 106		
XX	:::     :::		:::     :::
XX	320 GGTGCACACGCTAAATCATGTGTAATCCTCCAGATCCTGTGATGGCATG 369		
XX	107 AlahIsVallllelsAspll6olInPheGlyserGlnlleltysercy 123		
XX	:::     :::		:::     :::
XX	370 GTGCATCTGATCAAAGGCTCCAGCTGGATGCCAATAATTAATTCYTG 419		
XX	123 sProLYsgLyTYrArgleuIIeglySerSerSerAlatHrcysileles 140		
XX		:::	:::
XX	420 TACPAAMAGSATACCAGCATATGGTTCCTGCTGTCACATGCATCANCACT 469		
XX	140 ergIyaenThrallelrpaaspasnltyrhpProvalcysasp 154		
XX	:::		:::
XX	470 CAGGTGATCTGCTATTGGGATTAATAACACCTCTTTGTGTAC 513		
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seq_documentation_block:			
ID	AAQ11642 standard; DNA: 6951 BP.		
XX	AAQ11642;		
XX	25-JUN-1991 (first entry)		
DE	Entire human complement type 1 receptor coding region.		
KM	complement system; C3b/C4b receptor; CRI: allergic reaction;		
RW	immune response; clone lambda TI09.1; ss.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
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FT		/tag= a	
FT	mat_peptide	148..6144	
FT		/note= "putative"	
FT		/tag= b	
FT		/product= C3b/C4b receptor	
XX	WC9105047 -A.		

[illegible]

seq\_name: /STDS1/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:AAZ38150

seq\_documentation\_block:

ID AAZ38150 standard; DNA: 6951 BP.

AAZ38150;

22-FEB-2000 (first entry)

Human C3b/C4b receptor (CRL) protein encoding DNA.

C3B/C4B receptor; CRL protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; diagnostic; ss.

Homo sapiens.

US5961481.A.

09-NOV-1999.

06-JUN-1995; 9505-0470652.

03-APR-1989; 8905-0332865.

06-DEC-1974; 7405-0350248.

24-FEB-1993; 9305-0026134.

01-APR-1988; 8805-0176532.

(UYJO ) UNIV JOHNS HOPKINS.

(BGM ) BRIGHAM & WOMEN'S HOSPITAL.

(AVAN-) AVANT IMMUNOTHERAPEUTICS INC.

Concilio MF, Wong WM, Makrides SC, Klickstein LB, Fearon DF, Ip SH; Marsh HC, Carson GR;

WPI; 1999-633357/54.

P-PSDB: AAI55751.

A human C3b/C4b receptor (CRL) protein having anti-inflammatory and cardiant activity -

Disclosure: Fig 1A-P; 87pp; English.

The invention relates to a human C3B/C4b receptor (CRL) protein. The CRL protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full-length human CRL as expressed on erythrocytes. The CRL function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CRL protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRL protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CRL proteins, analogues, derivatives, and anti-CRL antibodies are used in assays, and diagnostics. The present sequence represents a DNA encoding the human CRL protein.

Sequence 6951 BP; 1802 A; 1680 C; 1661 G; 1808 T; 0 other;

alignment\_scores:  
 Quality: 649.50 Length: 148  
 Ratio: 4.883 Gaps: 2  
 Percent Similarity: 89.865 Percent Identity: 81.757

alignment\_block:  
 US-10-031-904-8 x AA158380 ..

Align seg 1/1 to: AA158380 from: 1 to: 6951

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10 ProPheProSerArgArgPhe.....ProGlyLeuLeuLeuAlaLale 24
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70 CCGGCGCCGCGGTCTCCCTTCTGCTGCGAGAGATCCCTGCTGCGGTTGT 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 GGTGCTGCTTGCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
40 rPLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
170 GGTCTTCATCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 lIleGlyThrTyrlLeuAsnTyrlGluCysArgProGlyTyrlSerGlyArgPr 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
220 ATGGGACATATCTGAACTATGAAATGCGCGCTGTTATTCGGAAGAC 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
73 oPheSerlleleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270 GTTTCTATCATCTGCTTAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 319
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90 yAcGlyLysArgLysSerCysArgAsnProProAspProValAsnGlyMet 106
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320 GGTGAGACGTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369
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107 AlaHisVallleLysAspIleGlnPheGlySerGlnIleLysTyrlSerG 123
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370 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
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123 sProlYsglyTyrlArgLeuIleGlySerSerSerAlaThrCysIlelle 140
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420 TACTTAAAGATACCGACTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
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140 erGlyAsnThrVallleTrpAspAsnLysThrProValCysAsp 154
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seq\_name: /SIDSL/gcgdata/geneseg/genesegn-emb1/NM2001A.DAT:AA158380

seq\_documentation\_block:  
 ID AA158380 standard; CDNA; 7313 BP.

AA158380;  
 22-OCT-2001 (first entry)  
 Human polynucleotide SEQ ID NO 583.  
 Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 Peripheral nervous system; neuropathy; central nervous system; CNS;  
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 leukemia; ss.  
 OS Homo sapiens.  
 XX  
 XX MO20015312-AL.  
 XX  
 XX 26-JUL-2001.  
 XX  
 XX 26-DEC-2000; 2000WO-US34263.  
 XX  
 XX

PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QH, Zhou P, Goorlich R, Demanac RT;

XX WPI: 2001-44253/47.  
 XX P-PSDB; AAM39224.

PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -

PS Claim 1; SEQ ID NO 583; 10078bp; English.

XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

SO Sequence 7313 BP; 1903 A; 1770 C; 1733 G; 1907 T; 0 other;

alignment\_scores:  
 Quality: 649.50 Length: 148  
 Ratio: 4.883 Gaps: 2  
 Percent Similarity: 89.865 Percent Identity: 81.757

alignment\_block:  
 US-10-031-904-8 x AA158380 ..

Align seg 1/1 to: AA158380 from: 1 to: 7313

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24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
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120 GGTGCTGCTTGCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 169
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40 rPLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
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170 GGTCTTCATTTGCGGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 219
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57 lIleGlyThrTyrlLeuAsnTyrlGluCysArgProGlyTyrlSerGlyArgPr 73
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220 ATGGGACATATCTGAACTATGAAATGCGCGCTGTTATTCGGAAGAC 269
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73 oPheSerlleleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
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140 SerGlyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154

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seq\_name: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA2001A.DAT:AA160166

seq\_documentation\_block:

ID AA160166 standard; cDNA: 7028 BP.

AA160166;

22-OCT-2001 (first entry)

Human polynucleotide SEQ ID NO 4155.

Human; nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;

KM peripheral nervous system; neuropathy; central nervous system; CNS;

KM Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;

KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KM chemokine; thrombolytic; drug screening; arthritis; inflammation;

KM leukaemia; ss.

OS Homo sapiens.

PN WO200153312-A1.

26-JUL-2001.

26-DEC-2000; 2000WO-US44263.

21-JAN-2000; 2000US-0488725.

25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.

19-JUL-2000; 2000US-0620312.

03-AUG-2000; 2000US-0653450.

14-SEP-2000; 2000US-0662191.

19-OCT-2000; 2000US-0693036.

29-NOV-2000; 2000US-0727344.

(HYSE-) HYSEQ INC.

Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

Wang J, Wang Z, Mehman T, Xu C, Xue AJ, Yang Y, Zhang J;

Zhao QA, Zhou P, Goodrich R, Dmanac RT;

WPI; 2001-442253/47.

P-PSDB; AAM41010.

Novel nucleic acids and polypeptides, useful for treating disorders

such as central nervous system injuries -

Claim 1; SEQ ID NO 4155; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and

the encoded polypeptides (AAM38642-AA44213) with nocitropic,

immunosuppressant and cytostatic activity. The polynucleotides are useful

in gene therapy. A composition containing a polypeptide or polynucleotide

system, such as peripheral nervous injuries, peripheral neuropathy and

localised neuropathies and central nervous system diseases, such as

Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

utilisation of the activities such as: immune system suppression,

activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic

and thrombolytic activity, cancer diagnosis and therapy, drug screening,

assays for receptor activity, arthritis and inflammation, leukaemia and

C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed

specification.

Sequence 7028 BP; 1819 A; 1704 C; 1681 G; 1824 T; 0 other;

alignment\_scores: Quality: 636.50 Length: 149

Ratio: 4.786 Gaps: 3

Percent Similarity: 89.262 Percent Identity: 81.208

alignment\_block:

US-10-031-904-8 x AA160166

Align seq 1/1 to: AA160166 from: 1 to: 7028

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70 CCGCGCCCGGTCCTCCCTCTGCGGAGATCCCTCTGCGGCTTGT 119

24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40

120 GGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 169

40 rpLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePr 56

170 GGGCTTCATTTGCCAGGCTACCACTCACTGATGATGATGATGAT 219

56 oileGlyThrTyrlLeuAsnTyrlCysArgProGlyTyrlSerGlyArgP 73

220 CATGGGACATATCTGAACATATGATGATGATGATGATGATGAT 269

73 ropPheSerIleIleCysLeuLysAsnSerValTrpPheSerAlaLysAsp 89

270 CGTTTCTATCATCTGCTTAAATAAAGTCACTGCTGCTGCTGCT 319

90 LysCysLysArgLysSerCysArgAspProPheProValAsnGlyMe 106

320 AGGTCAGACGTAATCATCTGATCTCTGATCTCTGATCTCTGAT 369

106 tAlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrlSerC 123

370 GGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 419

123 ySProlGlyTyrlArgLeuIleGlySerSerSerAlaThrCysIleIle 139

420 GTCCTAAGCATACCGACTATGTCCTGCTGCTGCACATGATC 469

140 SerGlyAsnThrValIleTrpAspAsnLysThrProValCysAsp 154

470 TCAGGTGATACGTCTGATTTGGATATGAAACACCATTTGTCAC 514

seq\_name: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV53262

seq\_documentation\_block:

ID AAV53262 standard; DNA: 591 BP.

AAV53262;

18-JAN-1999 (first entry)

Complement receptor type 1-like sequence CM7 DNA.

Complement receptor type-1; CRI; CM7; complement; inhibitor;

anti-haemolytic; multiple sclerosis; Parkinson's disease;

xenograft rejection; inflammation; Crohn's disease; asthma;

KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;

KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;

KM myasthenia gravis; reproductive disorder; therapy; ss.

OS Homo sapiens.

OS Synthetic.

PN WO9839433-A1.

PD 11-SEP-1998.

XX

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alignment_scores:      635.00      Length:      121
                      Quality:
                      Ratio:      5.336      Gaps:      0
Percent Similarity:    98.347      Percent Identity: 90.909
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US-10-031-904-8 x AAV53262

Align seg 1/1 to: AAV53262 from: 1 to: 591

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50  IAspAspPheGluIuAheProIleGluYThrTyrLeuAsnTyrGluCysArgP  67
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54  TGATGAAATTTAGTTAGTTCCTCCGATCGGCTACCTACTACCTACGAGATGGCGC  107

67  roGluTyrSerGluYArgProPheSerIleIleCysLeuYAsnSerVal  83
104  CGGGTTAATAGCGGGCGCCGCTTTTCATCACTACCTCCGAAAACACTGTGC  153

84  TyrThrSerAlaIalysAspLysCysLysArgLysSerLysArgAsnProPr  100
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154  TGGACGTGCGCTAAGAGACCGTTGCCGAGGTAAATCTTGCTAAATCCGC  203

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204 AGATCCGGTTAAAGGAGATGGTCATGTGATCAAAAGCAATCCAGTCGGTT 253
117 erghiiilvstyrsercysprolysglytyrargpaulleqlyser 133
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254 CCCAAATTAAATTTCTTGTACTAAAGGTACCGCTGATGTGGTTCCGCC 303
134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
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seq_documentation_block:
ID: 201603060 - standard.
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AAV53269 standard; DNA; 591 BP.

AC AAV53269;

DT 18-JAN-1999 (first entry)

DE Complement receptor type 1-like sequence CMI DNA

KW Complement receptor type-1; CR1; CMI; complement; inhibitor

KW xenograft rejection; inflammation; Crohn's disease; asthma;

autoimmune disease; rheumatoid arthritis; proliferative nephritis;

injacitura graviter, et proinde cito obdormit, incipit, ut  
XX

03 homo sapiens.  
05 Synthetic.

XX  
PN  
W09839433-A1

XX 11-SEP-1998  
PD

XX 05-MAR-1999: 08WD-GH00727  
DE

XX	0E-WAB-1007.	07CB-000AE10
DD		

XX

XX

[illegible]

DR P-P\$DB; AAW79237.

AA	PT	Soluble polypeptide
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97	97	97
98	98	98
99	99	99
100	100	100

PT used to treat disorders and diseases

XX  
PS  
Claim 22: Page 44: 67no: English

CC This DNA sequence encodes CM1 (see AAM79237), a protein that consists  
CC of the short consensus repeats (SCR) 1 and 2 from complement  
CC receptor type 1 (C1) fused to an SCR3 (see AAM79242) in which 5 amino  
CC acids were altered to those found in the SCR3 of the CRI-like  
CC pseudogene (Cripse) putative product. CM1 DNA was constructed by  
CC site-directed mutagenesis (see AAM53262) of plasmid pBD1013-5, which  
CC codes for SCR1-3 of C1. pBROSCR1-3CM1 carrying CM1 DNA was used  
CC to transform *Escherichia coli* BL21(DE3), and CM1 was purified from  
CC solubilised inclusion bodies. The invention provides DNA sequences  
CC (see AAM53262 and AAM53269-79) encoding novel soluble engineered CM1  
CC polypeptides (see AAM53266-47) such as CM1 that act as complement  
CC inhibitors with functional complement inhibitory, including  
CC anti-hemolytic, activity. These can be used to treat a disease or  
CC disorder associated with inflammation or inappropriate complement  
CC activation, such as neurological disorders (e.g. multiple sclerosis  
CC and Parkinson's disease), disorders of inappropriate or undesirable  
CC complement activation (e.g. xenograft rejection), inflammatory



CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC post-ischaemic reperfusion conditions, infection or sepsis,  
 CC immune complex disorders and autoimmune diseases (e.g. rheumatoid  
 CC arthritis, proliferative nephritis and myasthenia gravis), and  
 CC reproductive disorders.

XX Sequence 591 BP; 127 A; 159 C; 151 G; 154 T; 0 other;

alignment\_scores:                      Length:    121  
     Ratio:       5.336  
     Gaps:        0  
     Percent Similarity: 98.347    Percent Identity: 90.909

alignment\_block:  
 US-10-031-904-8 x AAV53269

Align seg 1/1 to: AAV53269 from: 1 to: 591

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50 rAspAspPheGluPheProIleGlyThrTrpLeuAsnTrpIleGlyAsp 67
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67 rGGLYrYrSerGlyArGProPheSerIleIleCysLeuLysAsnSerVal 83
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104 CGGGTATACGGCGCCCGCGTTTCTATACATGCTGCAAAACCTGCTC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 TrpTrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProp 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 rGAGATGCTCTAAGGACCGTTCGCGACGTAATCTTGCTAATCCGCC 203
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100 cAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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254 CCNAATTAATATATCTCTACTACTAAGTTACCGCTGATGTCCTCC 303
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seq\_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV53270

seq\_documentation\_block:  
 ID AAV53270 standard: DNA; 591 BP.

XX AAV53270:

XX 18-JAN-1999 (first entry)

XX Complement receptor type 1-like sequence CM2 DNA.

XX Complement receptor type-1; CRI; CM2; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy; ss.

XX Homo sapiens.  
 OS Synthetic.  
 XX

PN MO9839433-A1.

XX 11-SEP-1998.  
 PD 05-MAR-1998; 98MO-GB00727.  
 XX 05-MAR-1997; 97GB-0004519.  
 XX (ADPR-) ADPROTECH PLC.  
 XX Cox VE, Mossakowska DEI, Smith RAG.  
 XX WPI: 1998-506358/43.  
 XX P-PSDB; AAV79238.

XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
 XX used to treat disorders and diseases associated with inflammation or  
 XX inappropriate complement activation

XX Claim 22: Page 45; 67pp; English.

XX This DNA sequence encodes CM2 (see AAV79238), a protein that consists  
 XX of the short consensus repeats (SCR) 1 and 2 from complement  
 XX receptor type 1 (CRI) fused to an SCR3 (see AAV79243) in which 4 amino  
 XX acids were altered to those found in the SCR3 of the CRI-like  
 XX pseudogene (CrIpe) putative product. CM2 DNA was constructed by  
 XX site-directed mutagenesis (see AAV53264) of plasmid pDB103-5, which  
 XX codes for SCR1-3 of CRI pProSCR1-3CM2 carrying CM2 DNA was used  
 XX to transform *Escherichia coli* BL21(DE3), and CM2 was purified from  
 XX solubilised inclusion bodies. The invention provides DNA sequences  
 XX (see AAV53262 and AAV53269-79) encoding novel soluble engineered CRI  
 XX polypeptides (see AAV53236-47) such as CM2 that act as complement  
 XX inhibitors with functional complement inhibitory, including  
 XX anti-haemolytic, activity. These can be used to treat a disease or  
 XX disorder associated with inflammation or inappropriate complement  
 XX activation, such as neurological disorders (e.g. multiple sclerosis  
 XX and Parkinson's disease), disorders of inappropriate or undesirable  
 XX complement activation (e.g. xenograft rejection), inflammatory  
 XX disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 XX post-ischaemic reperfusion conditions, infection or sepsis,  
 XX immune complex disorders and autoimmune diseases (e.g. rheumatoid  
 XX arthritis, proliferative nephritis and myasthenia gravis), and  
 XX reproductive disorders.

XX Sequence 591 BP; 134 A; 158 C; 146 G; 153 T; 0 other;

alignment\_scores:                      Length:    121  
     Ratio:       5.336  
     Gaps:        0  
     Percent Similarity: 98.347    Percent Identity: 90.909

alignment\_block:  
 US-10-031-904-8 x AAV53270

Align seg 1/1 to: AAV53270 from: 1 to: 591

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50 rAspAspPheGluPheProIleGlyThrTrpLeuAsnTrpIleGlyAsp 67
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67 rGGLYrYrSerGlyArGProPheSerIleIleCysLeuLysAsnSerVal 83
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154 rGAGATGCTCTAAGGACCGTTCGCGACGTAATCTTGCTAATCCGCC 203
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100 cAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 117
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|||||
204 AGATCGGTTAAGCAGTCATGATGATCAAGCAGTCGCTT 253
117 erglnlleltyrsercysprolysglytyrargleuileglyserSer 133
254 CCCAAATTAAATTTCTTCTACTAAAGTACCGTCTGATTCCTCC 303
134 SerAlaThrCysTlleIleSerGlyAspThrValIleThrPAsnLysTh 150
304 ACCGCTACATGCATCATCTCTGTGATCTCATTTGGATATGAAAC 353
150 rProValCysAsp 154
|||||
354 ACCGATTGTGAC 366

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV53271
seq_documentation_block:
ID AAV53271 standard; DNA; 591 BP.
XX
AC AAV53271;
XX
DT 18-JAN-1999 (first entry)
XX
DE Complement receptor type 1-like sequence CM3 DNA.
NM Complement receptor type-1; CRI; CM3; complement; inhibitor;
anti-haemolytic; multiple sclerosis; Parkinson's disease;
xeno-graft rejection; inflammation; Crohn's disease; asthma;
pancreatitis; post-ischaemic reperfusion; infection; sepsis;
autoimmune disease; rheumatoid arthritis; proliferative nephritis;
myasthenia gravis; reproductive disorder; therapy; ss.
XX
OS Homo sapiens.
XX
SY Synthetic.
XX
PN MO9839433-A1.
XX
PD 11-SEP-1998.
XX
PE 05-MAR-1998; 98MO-GB00727.
XX
PR 05-MAR-1997; 97GB-0004519.
XX
PA (ADPR-) ADPROTECH PLC.
PI Cox VF, Mossakowska DEI, Smith RAG;
XX
XX WPI: 1998-506358/43.
XX P-PSDB; AAW9239.
XX
DR Soluble polypeptide comprising short consensus repeats from LHR-A -
XX used to treat disorders and diseases associated with inflammation or
XX inappropriate complement activation
XX
XX Claim 22; Page 46; 67pp; English.
XX
XX This DNA sequence encodes CM2 (see AAW9239), a protein that consists
XX of the short consensus repeats (SCR) 1 and 2 from complement
XX receptor type 1 (CRI) fused to an SCR3 (see AAW9244) in which 1 amino
XX acid was altered to that found in the SCR3 of the CRI-like
XX pseudogene (Cr1pse) putative product. CM3 DNA was constructed by
XX site-directed mutagenesis (see AAV53265) of plasmid pBI013-5, which
XX codes for SCR-3 of CRI. pBROSOCR1-3CM3 carrying CM3 DNA was used
XX to transform Escherichia coli BL21(DE3), and CM3 was purified from
XX subcloned inclusion bodies. The invention provides DNA sequences
XX (see AAV53262 and AAV53269-79) encoding novel soluble engineered CRI
XX polypeptides (see AAW53236-47) such as CM3 that act as complement
XX inhibitors with functional complement inhibitory, including
XX anti-haemolytic, activity. These can be used to treat a disease or
XX disorder associated with inflammation or inappropriate complement
XX activation, such as neurological disorders (e.g. multiple sclerosis
XX and Parkinson's disease), disorders of inappropriate or undesirable

```

```

CC complement activation (e.g. xenograft rejection), inflammatory
CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),
CC post-ischaemic reperfusion conditions, infection or sepsis,
CC immune complex disorders and autoimmune diseases (e.g. rheumatoid
CC arthritis, proliferative nephritis and myasthenia gravis), and
CC reproductive disorders.
XX
SQ Sequence 591 BP; 131 A; 160 C; 149 G; 151 T; 0 other;

alignment_scores:
Quality: 635.00 Length: 121
Ratio: 5.336 Gaps: 0
Percent Similarity: 98.347 Percent Identity: 90.909

alignment_block:
US-10-031-904-8 x AAV53271 ..
Align seg 1/1 to: AAV53271 from: 1 to: 591

34 GlucyAsnValProGluThrLeuProPheAlaArgProThrAsnLeuTh 50
|||||
4 CAGTCACACGCTCCGGAATGCTGCGCTCCGCGCCGACCACTGAC 53
50 rAspAspPheGluPheProIleGlyThrIleuAsnTyrgLucysArgp 67
|||||
54 TCATGAAATTTGAGTTCCTCCGATCGGATCCCTGAACTGACGAATGCGCC 103
67 roGlyTyrsSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
|||||
104 CCGGTTATAGCGGCCGCCGCTTTCTATCATCTGCGCTGAAAACCTGTC 153
84 TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProp 100
|||||
154 TCGACTGTGCTGACGAGCCGCTTCCGACGTAATCTTTCGAAATCCGCC 203
100 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 117
|||||
204 ACATCCGGTTAAGCAGTCATGATGATCAAGCAGCATCCGATCGGTT 253
117 erglnlleltyrsercysprolysglytyrargleuileglyserSer 133
|||||
254 CCCAAATTAAATTTCTTCTACTAAAGTACCGTCTGATTCCTCC 303
134 SerAlaThrCysTlleIleSerGlyAspThrValIleThrPAsnLysTh 150
|||||
304 ACCGCTACATGCATCATCTCTGTGATCTCATTTGGCATATGAAAC 353
150 rProValCysAsp 154
|||||
354 ACCGATTGTGAC 366

seq_name: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:AAV53272
seq_documentation_block:
ID AAV53272 standard; DNA; 591 BP.
XX
AC AAV53272;
XX
DT 18-JAN-1999 (first entry)
XX
DE Complement receptor type 1-like sequence CM5 DNA.
XX
XX Complement receptor type-1; CRI; CM5; complement; inhibitor;
XX anti-haemolytic; multiple sclerosis; Parkinson's disease;
XX xeno-graft rejection; inflammation; Crohn's disease; asthma;
XX pancreatitis; post-ischaemic reperfusion; infection; sepsis;
XX autoimmune disease; rheumatoid arthritis; proliferative nephritis;
XX myasthenia gravis; reproductive disorder; therapy; ss.
XX
XX Homo sapiens.
XX
XX Synthetic.

```

PN W09839433-A1.  
 XX 11-SEP-1998.  
 PD 05-MAR-1998; 98WO-GB00727.  
 XX 05-MAR-1997; 97GB-0004519.  
 PR (ADPR-) ADPROTECH PLC.  
 PA Cox VF, Mossakowska DEL, Smith RAG;  
 PI MPI: 1998-506358/43.  
 DR P-PSDB; AAW79240.  
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
 used to treat disorders and diseases associated with inflammation or  
 inappropriate complement activation  
 Claim 22; Page 47; 67pp; English.  
 XX This DNA sequence encodes CM5 (see AAW79240), a protein that consists  
 CC of the short consensus repeats (SCR) 1 and 2 from complement  
 CC receptor type 1 (CRI) fused to an SCR3 (see AAW79240) in which 5 amino  
 CC acids were altered to those found in the SCR3 of the CRI-like  
 CC pseudogene (Cripse) putative product. CM5 DNA was constructed by  
 CC site-directed mutagenesis (see AAW53264-65) of pDB1013-5 which  
 CC codes for SCR1-3 of CRI. pProSCR1-3CM5 carrying CM5 DNA was used  
 CC to transform *Escherichia coli* BL21(DE3), and CM5 was purified from  
 CC solidified inclusion bodies. The invention provides DNA sequences  
 CC (see AAW53262 and AAW53269-79) encoding novel soluble engineered CRI  
 CC polypeptides (see AAW53264-47) such as CM5 that act as complement  
 CC inhibitors with functional complement inhibitory, including  
 CC anti-haemolytic, activity. These can be used to treat a disease or  
 CC disorder associated with inflammation or inappropriate complement  
 CC activation, such as neurological disorders (e.g. multiple sclerosis  
 CC and Parkinson's disease), disorders of inappropriate or undesirable  
 CC complement activation (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC post-ischaemic reperfusion conditions, infection or sepsis,  
 CC immune complex disorders and autoimmune diseases (e.g. rheumatoid  
 CC arthritis, proliferative nephritis and myasthenia gravis), and  
 CC reproductive disorders.  
 S0 Sequence 591 BP; 128 A; 160 C; 151 G; 152 T; 0 other;  
 alignment\_scores:                   Length: 121  
                   Quality: 635.00                   Gaps: 0  
                   Ratio: 5.336                    Percent Identity: 90.909  
 Percent Similarity: 98.347  
 alignment\_block:  
 US-10-031-904-8 x AAW53272 ..  
 Align seg 1/1 to: AAW53272 from: 1 to: 591  
 34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50  
 4 CAGTGCACGCTCCGGAATGCTCCCTTCGCGCCGCAACACACCTGAC 53  
 50 TASPAPPhagLupheProIleGlyTrpTyrLeuAsnTyrGluCysArgP 67  
 54 TGAATGAATTGAGTCCGATCGGTACCTGACCTGACCTGACCTGACCTG 103  
 67 rogllyrSerGlyArpProPheSerIleIleCysLeuAsnSerAla 83  
 104 CGGGTATAGCGCCGCCGCTTTCTATCATCTGCTGAAAAACHTGTG 153  
 84 TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProP 100  
 154 TGGACGTGCTGTAAGACCGTTCGCGACGTAAATCTTGTGTAATCCGCC 203

100 oAsProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117  
 204 AGATCGGCTAACGCGCATGGTCATGTGATCAAGACATCCAGTCCGCTT 253  
 117 ergGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133  
 254 CCAAAATTAATTAATCTTGTGTAAGTACCGCTGCTGATGGTGTCC 303  
 134 SerAlaTrpCysIleIleSerGlyAsnTrpValIleTrpAspAsnLysTrp 150  
 304 AGCGCTACATGCATCATCTCTGATGATCTGATCTGATGATGATGAAC 353  
 150 rProValCysasp 154  
 354 ACCGATTTGTGAC 366  
 seq\_name: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1998.DAT:AAW53273  
 seq\_documentation\_block:  
 ID AAW53273 standard; DNA; 591 BP.  
 AC AAW53273:  
 XX 18-JAN-1999 (first entry)  
 XX  
 DE Complement receptor type 1-like sequence CM6 DNA.  
 XX  
 KM Complement receptor type-1; CRI; CM6; complement; inhibitor;  
 KM anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KM xenograft rejection; inflammation; Crohn's disease; asthma;  
 KM pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KM myasthenia gravis; reproductive disorder; therapy; ss.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS  
 PN W09839433-A1.  
 PD 11-SEP-1998.  
 XX 05-MAR-1998; 98WO-GB00727.  
 XX 05-MAR-1997; 97GB-0004519.  
 XX (ADPR-) ADPROTECH PLC.  
 PA Cox VF, Mossakowska DEL, Smith RAG;  
 PI MPI: 1998-506358/43.  
 DR P-PSDB; AAW79241.  
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
 used to treat disorders and diseases associated with inflammation or  
 inappropriate complement activation  
 Claim 22; Page 48; 67pp; English.  
 XX This DNA sequence encodes CM6 (see AAW79241), a protein that consists  
 CC of the short consensus repeats (SCR) 1 and 2 from complement  
 CC receptor type 1 (CRI) fused to an SCR3 (see AAW79240) in which 6 amino  
 CC acids were altered to those found in the SCR3 of the CRI-like  
 CC pseudogene (Cripse) putative product. CM6 DNA was constructed by  
 CC site-directed mutagenesis (see AAW53263 and AAW53265) of pDB1013-5,  
 CC which codes for SCR1-3 of CRI. pProSCR1-3CM6 carrying CM6 DNA was used  
 CC to transform *Escherichia coli* BL21(DE3), and CM6 was purified from  
 CC solidified inclusion bodies. The invention provides DNA sequences  
 CC (see AAW53262 and AAW53269-47) such as CM6 that act as complement  
 CC inhibitors with functional complement inhibitory, including  
 CC anti-haemolytic, activity. These can be used to treat a disease or  
 CC disorder associated with inflammation or inappropriate complement  
 CC activation, such as neurological disorders (e.g. multiple sclerosis

CC and Parkinson's disease), disorders of inappropriate or undesirable  
 CC complement activation (e.g. xenograft rejection), inflammatory  
 CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC post-ischemic reperfusion conditions, infection or sepsis,  
 CC immune complex disorders and autoimmune diseases (e.g. rheumatoid  
 CC arthritis, proliferative nephritis and myasthenia gravis), and  
 CC reproductive disorders.

Sequence 591 BP; 135 A; 159 C; 146 G; 151 T; 0 other;

#### alignment\_scores:

Quality: 635.00 Length: 121  
 Ratio: 5.336 Gaps: 0  
 Percent Similarity: 98.347 Percent Identity: 90.909

#### alignment\_block:

US-10-031-904-8 x AAV53273 ..

Align seq 1/1 to: AAV53273 from: 1 to: 591

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34 GlnCysAsnValProGluTyrPheProPheAlaArgProThrAsnLeuTh 50
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4 CAGTGCACGCTCCGGAATGGCTGCCGTCGCCGCCGACCACTGAC 53
50 TASPAPhpeGluPheProIleGlyTyrTyrLeuAsnTyrGluCysArgP 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
54 TGAATGATTTGAGTCCGATGGGACCTGACCTGAACCTGAGAAATGCCGC 103
67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnVal 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
104 CGGGTTATAGCGCGCCCGCTTTCTATCATCTGCTGAAAAACTCTGTG 153
84 TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
154 TGGACGTGGTGTAGAGACCGTTGCCGAGTAAATCTTGTCGTAATCCGCC 203
100 oASPProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
204 AGATCCGGTTACGGATGGTGCATGTGATCAAGCATCCAGTCTGGTT 253
117 erGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
254 CCAAAATTAATATCTTGTACTAAAGGTACCGTCTGATGTGCTCTCC 303
134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
304 AGCGTACATGCATCATCTGCTGATACATCTCTTTGGGATATGAAAC 353
150 rProValCysAsp 154
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
354 ACCGATTTGTGAC 366

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seq\_name: /SIDSL/9cdata/geneseq/geneseq-emb1/NA1993.DAT:AAQ41867

seq\_documentation\_block:

ID AAQ41867 standard; DNA; 6951 BP.

AAQ41867:

14-SEP-1993 (first entry)

CRI coding region.

C3b/C4b receptor; CRI, erythrocyte; monocyte; macrophage; granulocyte;  
 1G3b; T cell; splenic follicular dendritic cell; soluble; complement;  
 glomerular podocyte; B cell; C3b; C4b; inactivated C3b; phagocytosis;  
 plasma; ligand binding activity; immune complex; activator; allotype;  
 endocytosis; lymphocyte; classical; alternative; pathway; cofactor; F  
 C3/C5 convertase; liver; cleavage; factor I; regulation; glycoprotein;  
 S; A; B; glycosylation; duplication; repetitive intervening sequence;  
 endoglycosidase F; ss.

OS Homo sapiens.

XX	Key	Location/Qualifiers
XX	CDS	28..6147
XX	sig_peptide	28..150
XX	mat_peptide	151..6144
XX	misc_RNA	1534..6147
XX	misc_difference	509..512
XX	note="CRL CDNA"	
XX	note="Unclear in the specification"	

US5212071-A.

18-MAY-1993.

01-APR-1988; 88US-0176532.

01-APR-1988; 88US-0176532.

03-APR-1989; 89US-0332865.

(BCHM) BRIGHAM & WOMENS HOSPITAL.

(TECL-) T CELL SCI INC.

(UYO) UNIV JOHN HOPKINS.

Carson GR, Concino ME, Fearon DT, Ip SH, Klickstein LB;

Makrides SC, Wong WW;

P-PSDB; AAR36743.

WPI; 1993-175454/21.

Nucleic acid encoding polypeptide having complement regulatory

activity - used to prevent reperfusion injury, inhibit Arthus

reaction and neutrophil mediated tissue damage and reduce

myocardial infarct size and inflammation

Claim 1: Fig 1; 90pp; English.

This sequence represents the entire coding region for the C3b/C4b  
 receptor (CRI). CRI is present on erythrocytes, monocytes/macro-  
 phages, granulocytes, B cells, some T cells, splenic follicular  
 dendritic cells and glomerular podocytes. CRI specifically binds  
 C3b, C4b and inactivated C3b (iC3b). A soluble form of the receptor  
 is found in plasma which has ligand binding activity and the same  
 molecular weight as membrane-associated CRI. CRI binds C3b and C4b  
 that have covalently attached to immune complexes and other complement  
 activators. The consequences of these interactions depends on the  
 type of bearing the receptor. Erythrocyte CRI binds immune complexes  
 for transport to the liver. CRI on neutrophils and monocytes  
 internalises bound complexes, either by adsorptive endocytosis  
 or by phagocytosis. The function of CRI on B lymphocytes is less  
 well defined. CRI can inhibit the classical and alternative pathway  
 C3/C5 convertases and act as a cofactor for the cleavage of C3b and  
 C4b by factor I, therefore CRI has a complement regulatory function  
 as well as acting as a receptor. CRI is a glycoprotein composed of  
 a single polypeptide chain. Four allotypic forms of CRI have been  
 identified, differing by increments of approx. 40-50 kD. The two most  
 common forms, the F and S allotypes, also termed A and B allotypes,  
 have molecular weights of 250 and 290 kD respectively. The two rarer  
 CC forms have molecular weights of 210 and 290 kD. These differences  
 represent differences in the polypeptide chain of CRI, rather than  
 glycosylation state because they are not abolished by treatment of  
 CC purified receptor protein with endoglycosidase F. The CRI gene has  
 CC been shown to have repetitive intervening sequences which may have  
 CC been duplicated in the formation of the larger allotypes.

Sequence 6951 BP; 1799 A; 1692 C; 1648 G; 1807 T; 5 other;

alignment\_scores:  
Quality: 634.50 Length: 146  
Ratio: 4.844 Gaps: 2  
Percent Similarity: 89.726 Percent Identity: 81.507

alignment\_block:  
US-10-031-904-8 x AAQ41867 ..

Align seg 1/1 to: AAQ41867 from: 1 to: 6951

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70 CGGGGGCCCGCTCCCTCTGCTGCGGAGATCCCTGCTGCGGCTTGT 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGlu 40
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 GGTGCTGCTGCTGCGGCTGCGGCTGCGGCTGCAATGCAATGCCAGAA 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
40 rPLeuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
170 GGCCTTCATTTGCCAGGCTTACCACTTACCTTACCTTACCTTACCTT 219
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 lIeGlyThrTyLeuAsnTyGluCysArgProGlyTyrSerGlyArgPr 73
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
220 ATTGGGACATATCTGAACATATGAATGCCGCCCTGCTTATTCGGAAAG 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
73 oPheSerIleIleCysLeuLysAsnSerValTTrPThrSerAlaLysAsp 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270 GTTTCTTCTCATCTGCTCTAAATAAATCTAGTCTGACTGGTGTAAAGACA 319
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
90 yScysLysArgLysSerCysArgAsnProProAspProValAsnGlyMet 106
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
320 GGTGCAGACGTAAATCATGTCGTATCTCCAGATCTCTGGAATGGCARG 369
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
107 AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
   ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
370 GTGCATGTGATCAAAAGGATCCAGTTCGATCCCAATTAATATTTCTTG 419
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaIleThrCysIleIle 140
   | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
420 TACTAAAGGATACCGACATCATTTGCTTCTGCTGCTGCTGCTGCTGCT 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
140 eRGlyAsnThrValIleTrpAspAsnLysThrProVal 152
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Align seg 1/1 to: HSCR18S from: 1 to: 2376

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   |||||.....|||
56 CAATGCCCGAGAAATGGCTTCATTTGCCAGGCTACCACTAATCATGATG 105
   |||||.....|||
52 sPheGluPheProIleGlyThrTyrLeuAsnTyrGlnCysArgProGly 68
   |||||.....|||
106 AGTTTGAGTTTCCCATTTGGGACATATCTGAACATGATGATGCCGCCCTG 155
   |||||.....|||
69 TyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerValTrpTh 85
   |||||.....|||
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   |||||.....|||
85 rSerAlaLysAspLysCysLysArgLysSerCysArgAsnProProAsp 102
   |||||.....|||
206 TGGTGCTTAAGACAGGTGCAGACGTAAATCATGTGTAATCTCTCAGATC 255
   |||||.....|||
102 roValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlySerGln 118
   |||||.....|||
256 CTGTGAATGGCATGTGTCATGTGATCAAAAGGCATCCAGTTGCGATCCCA 305
   |||||.....|||
119 IleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSerAl 135
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306 ATTAATAATCTCTGTACTAAAGATACCGACTCATGTGCTCTGCTGTCG 355
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seq\_name: gb\_sts:G28591

seq\_documentation\_block:

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LOCUS       G28591                2376 bp    DNA    linear    STS 11-JUL-1996
DEFINITION human STS SHGC-35372, sequence tagged site.
ACCESSION  G28591
VERSION    G28591.1 GI:1408406
XREFS     STS: STS sequence; primer; sequence tagged site.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 2376)
AUTHORS   Myers, R.M.
JOURNAL   Unpublished
COMMENT   Contact: Richard M. Myers
          Stanford Human Genome Center (SHGC)
          Stanford University School of Medicine
          Department of Genetics, M-344, Stanford, CA 94305, USA
          Tel: 415/7258687
          Fax: 415/7259689
          Email: myers@shgc.stanford.edu

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Primer A: TGAGTTGGACGACATGTC  
Primer B: CATACTCTTATATGTGCACCTGCC  
STS size: 216  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR cycles: 30  
Thermal Cycler: Perkin Elmer 9600

# Protocol:

Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/ul  
Total Vol: 10 ul

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from X14362  
-- Washington University/Merck EST sequence.

FEATURES  
source  
1. .2376  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

STS  
primer\_bind 1680..1895  
1680..1699  
primer\_bind complement(1672..1895)  
BASE COUNT 633 a 549 c 568 g 626 t  
ORIGIN

alignment\_scores:  
Quality: 644.50 Length: 136  
Ratio: 5.035 Gaps: 1  
Percent Similarity: 94.118 Percent Identity: 86.029

alignment\_block:  
US-10-031-904-8 x G28591 ..

Align seg 1/1 to: G28591 from: 1 to: 2376

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20 LeuLeuAlaLeuValLeuLeu...LeuSerSerPheSerAspGlnGly 35
   |||||.....|||
6  CTGCTGCGGCTTGTGTGCTGCTGCGCTGCCGTGGCTGGGCTCAATG 55
   |||||.....|||
35 sAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThrAsp 52
   |||||.....|||
56 CAATGCCCGAGAAATGGCTTCATTTGCCAGGCTACCACTAATCATGATG 105
   |||||.....|||
52 sPheGluPheProIleGlyThrTyrLeuAsnTyrGlnCysArgProGly 68
   |||||.....|||
106 AGTTTGAGTTTCCCATTTGGGACATATCTGAACTATGATGACCGCCTGGT 155
   |||||.....|||
69 TyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerValTrpTh 85
   |||||.....|||
156 TATTCGGGAAGACCGTTTTCATCATCTGCCCTAAAAAACACAGCTGAGAC 205
   |||||.....|||
85 rSerAlaLysAspLysCysLysArgLysSerCysArgAsnProProAsp 102
   |||||.....|||
206 TGGTGCTTAAGACAGGTGCAGACGTAAATCATGTGTAATCTCTCAGATC 255
   |||||.....|||
102 roValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlySerGln 118
   |||||.....|||
256 CTGTGAATGGCATGTGTCATGTGATCAAAAGGCATCCAGTTGCGATCCCA 305
   |||||.....|||
119 IleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSerAl 135
   |||||.....|||
306 ATTAATAATCTCTGTACTAAAGATACCGACTCATGTGCTCTGCTGTCG 355
   |||||.....|||
135 aThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrProV 152
   |||||.....|||
356 CACATGGCATCATCTCAGGTGATCTGTCATTTGGGATTAATGAACACCTA 405
   |||||.....|||
152 aLcysAsp 154
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406 TTTGTGAC 413

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alignment\_block:  
US-10-031-904-8 x A86607

Align seg 1/1 to: A86607 from: 1 to: 591

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34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 CAGTGCACACGCTCCGGAATGGCTGCGCGCCGCCGCCACCAACCTGAC 53
50 RAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
54 TGATGATTTGAGTTCGCCATCGGTCACCTGACCTGAACCTACGATCCGCC 103
67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
104 CGGGTTATACGGCGCCCGCTTTTCATCATCTGCTCAAAAACCTGCTC 153
84 TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 TGACACTGCTCTAAGACCGCTGCCGACGTAAATCTTGCTGTAATCCGCC 203
204 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 AGATCCGGTTAACGGCATGTCATGATCAAGCATCCAGTTCCGGTT 253
117 ergInIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 CCAAAATTAAATATTCTTGTACTAAAGTTACCGTCTGATTTGTTCCCTC 303
134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 AGCGCTACATGCATCATCTCTGTGATCTGATCTGATTTGGATTAATGAAC 353
150 rProValCysAsp 154
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354 ACCGATTGTGAC 366

```

seq\_name: gb\_pat:A86609

seq\_documentation\_block:

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LOCUS      A86609                      591 bp    DNA     linear    PAT 21-JAN-2000
DEFINITION Sequence 18 from Patent WO9839433.
ACCESSION  A86609
VERSION    A86609.1 GI:6735179
KEYWORDS   .
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 591)
AUTHORS   Smith, R.A. and Cox, V.F.
TITLE     COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL   Patent: WO 9839433-A 18 11-SEP-1998;
          SMITH RICHARD ANTONI GODWIN (GB); ADPROTECH PLC (GB)
FEATURES   source
            1..591
            /organism="unidentified"
            /db_xref="taxon:32644"
BASE COUNT 135 a 159 c 146 g 151 t
ORIGIN

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alignment\_scores:  
Quality: 635.00 Length: 121  
Ratio: 5.336 Gaps: 0  
Percent Similarity: 98.347 Percent Identity: 90.909

alignment\_block:

US-10-031-904-8 x A86609

Align seg 1/1 to: A86609 from: 1 to: 591

34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50

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|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
4 CAGTGCACACGCTCCGGAATGGCTGCGCGCCGCCGCCACCAACCTGAC 53

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```

50 RAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
54 TGATGATTTGAGTTCGCCATCGGTCACCTGACCTGAACCTACGATCCGCC 103
67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
104 CGGGTTATACGGCGCCCGCTTTTCATCATCTGCTCAAAAACCTGCTC 153
84 TrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPr 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
154 TGACACTGCTCTAAGACCGCTGCCGACGTAAATCTTGCTGTAATCCGCC 203
204 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGlyS 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 AGATCCGGTTAACGGCATGTCATGATCAAGCATCCAGTTCCGGTT 253
117 ergInIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 CCAAAATTAAATATTCTTGTACTAAAGTTACCGTCTGATTTGTTCCCTC 303
134 SerAlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysTh 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
304 AGCGCTACATGCATCATCTCTGTGATCTGATCTGATTTGGATTAATGAAC 353
150 rProValCysAsp 154
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
354 ACCGATTGTGAC 366

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seq\_name: gb\_pat:AR029199

seq\_documentation\_block:

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LOCUS      AR029199                      605 bp    DNA     linear    PAT 29-SEP-1999
DEFINITION Sequence 33 from patent US 5859223.
ACCESSION  AR029199
VERSION    AR029199.1 GI:5941172
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 605)
AUTHORS   Mossakowska, D. Ewa-Irena., Dodd, I., Freeman, A. Mary. and
          Soluble CR1 derivatives.
TITLE     Patent: US 5859223-A 33 12-JAN-1999;
JOURNAL   Location/Qualifiers
FEATURES   source
            1..605
            /organism="unknown"
BASE COUNT 136 a 161 c 150 g 158 t
ORIGIN

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alignment\_scores:  
Quality: 635.00 Length: 121  
Ratio: 5.336 Gaps: 0  
Percent Similarity: 98.347 Percent Identity: 90.909

alignment\_block:

US-10-031-904-8 x AR029199

Align seg 1/1 to: AR029199 from: 1 to: 605

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34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
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7 CAGTGCACACGCTCCGGAATGGCTGCGCGCCGCCGCCACCAACCTGAC 56
50 RAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgP 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57 TGATGATTTGAGTTCGCCATCGGTCACCTGACCTGAACCTACGATCCGCC 106
67 roGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83

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```
|||||
107 CCGGTTATAGCGCGCCGGTTTCTATCATCTGCGTAAAACTCTGTC 156
84 TrrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAspProp 100
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157 TGGACTGGCTAAGGACCGTTGCCGTAATCTTGTCTGTAATCCGCC 206
100 oAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 117
|||||
207 AGATCCGGTTACGGCATGCTCATGTGTAAGGCAATCCAGTTCCGTT 256
117 eGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSer 133
|||||
257 CCCAATTAATATCTTGTACTAAGGTACCGCTGATGTTCTCTCC 306
134 SerAlaThrCysIleLeSerGlyAsnThrValIleTrrPaspAsnLys 150
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307 ACCGCTACATGCATCATCTGTGTATCATGTGCATTGGGATTAATGAAC 356
150 rProValCysAsp 154
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357 ACCGATTCTGTGAC 369

seq_name: gb_pr:BABCORE
seq_documentation_block:
LOCUS BABCORE 1688 bp mRNA linear PRI 07-MAY-1996
DEFINITION Papio cynocephalus complement receptor mRNA, partial cds.
ACCESSION L77977
VERSION L77977.1 GI:1301608
KEYWORDS complement C3b; complement receptor;
glycophosphatidylinositol-linked protein.
SOURCE Papio cynocephalus cDNA to mRNA.
ORGANISM Papio cynocephalus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopithecinae; Papio.
1 (bases 1 to 1688)
REFERENCE Birmingham,D.J., Logar,C.M., Shen,X.-P. and Chen,W.
TITLE The baboon erythrocyte complement receptor is a glycosphosphatidyl
inositol-linked protein encoded by a homologue of the human
CRI-like genetic element
JOURNAL Unpublished (1996)
FEATURES
location/Qualifiers
source
1..1688
/organism="Papio cynocephalus"
/db_xref="taxon:9536"
/cell_type="erythrocyte"
/tissue_type="bone marrow"
/dev_stage="adult"
<1..>1688
<1..1571
/note="homologue of human CRI-like genetic element"
/codon_start=3
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/protein_id="AAA99004.1"
/db_xref="GI:1301608"
/translacion="VVIQKRGASSPSPPEVGPAPRLFFCCGSLAVVLLALPVA
WGOCNAPEQLPFAPIPLIDASEFPVGTIRKCLPQYHAKPSIICLNKSWTSKD
KCTRKSCRNPKDPVNGVAVHVKIDIOGSOYNKNGYRLIGSSATCIISGNTVMD
NETPICIEIIPGGLPTIANGDFISTREYPPYSVYTRCNLSGRRKLEELGEPST
YCTSKDOVQIWSGPAPOCIIPNKCMPNPNVAVNSLFLSLNDVEFCOPGF
MKGPRIYCOALKNKEBELPSCRVPCOPREIILAGHTPSHODPSGQEVYSCEBGY
DLRGASLHCTPGQDNKPEAPICTVYSCDFLQCLPHGRVLFPLNQLQAKVSFVDE
GFRKGRFASHCVIAGKALMNSVPCVEQIFCPNPAILNGRHIAPIGLDIPYGKEL
SYICDPHDPGRGMTVNLIGESTIRCTSDPOGNSWSPAPRCELSVPAGANDALIVGTL
SGTIFVLIETIFLS"
BASE COUNT 413 a 427 c 411 g 437 t
ORIGIN
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alignment\_scores: 599.50 Length: 138

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Ratio: 4.874 Gaps: 1
Percent Similarity: 89.130 Percent Identity: 81.159
alignment_block:
US-10-031-904-8 x BABCORE ..
Align seg 1/1 to: BABCORE from: 1 to: 1688
18 GlyLeuLeuAlaAlaLeuValLeu...LeuSerSerPheSerAs 33
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90 GGATCCCTGTTGGCGGTTGTGTCTGCTCGCGTGCCTGAGCTGGGG 139
33 pGlnCysAsnValProGluTrrPleuProPheAlaArgProThrAsnLeu 50
|||||
140 TCATATGCAATGCCCGGACAGCTTCATTTGCCAGGCTACCACTTA 169
50 hrAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArg 66
|||||
190 CTGATGCATCTGAGTTCCTCCGTTGGACATATCTGAAGTATGATGCTC 239
67 ProGlyTyrSerGlyArgProPheSerIleLeuCysLeuLysAsnSerVa 83
|||||
240 CTTGTTATCATGGAGAAACCATTTCTATCATCTGCTTAATAAACTAGT 289
83 lTrrPThrSerAlaLysAspLysCysLysArgLysSerCysArgAspProp 100
|||||
290 CTGACAAAGTCTCTAAGGACAAAGTCACACGTAATATCATGCTAATCT 339
100 rAspProValAsnGlyMetAlaHisValIleLysAspIleGlnPheGly 116
|||||
340 AAGATCTGTGTAAGGATGCTGATGATCAAGACATCCAGTTCGGA 389
117 SerGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSe 133
|||||
390 TCCCAATTAATATTCTTGTATTAAGATACGATCATGTTGTTCTTC 439
133 rSerAlaThrCysIleLeSerGlyAsnThrValIleTrrPaspAsnLys 150
|||||
440 GTCCGCCACATGATCATCATCAGGCATACATGTTGGGATATGAAA 489
150 hrProValCysAsp 154
|||||
490 CACCTATTGTGAG 503

seq_name: gb_pr:BABCR1A
seq_documentation_block:
LOCUS BABCR1A 6000 bp mRNA linear PRI 11-FEB-1995
DEFINITION Papio hamadryas complement component receptor type 1 (CRI) mRNA,
complete cds.
ACCESSION L39791
VERSION L39791.1 GI:662828
KEYWORDS C3b/C4b complement component receptor; complement component
receptor CRI; complement receptor 1.
SOURCE Papio hamadryas (clone SPC-CYT3NC) cDNA to mRNA.
ORGANISM Papio hamadryas
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopithecinae; Papio.
1 (bases 1 to 6000)
REFERENCE Clemenz,L., Subramanian,B.V., Nickells,M.W., Hourcade,D.E. and
ATTIKSON,J.P.
TITLE Primary sequence of the baboon 200 kDa C3b/C4b receptor (CRI)
JOURNAL Unpublished (1995)
FEATURES
location/Qualifiers
source
1..6000
/organism="Papio hamadryas"
/db_xref="taxon:9557"
/clone="SPC-CYT3NC"
/cell_line="26CB-1"
/cell_type="lymphoblastoid"
1..6000
/gene="CRI"
gene
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403 AACGATGACTTTGAGTTCCCATTTGGGACATATCTAATGATGATGCC 354
66 rprpogl1tyrserglyarpropheserlelleleuylsasnser 82
353 GCCCTGGTATTCCGGAAGACCGTTTCTATCATCTGCCATTAATACTCA 304
83 Val1rprp1tyrserglyarpropheserlelleleuylsasnser 99
303 GTCCTGACAAAGTCTTAAGACAACTGCAACGTAATCAATCTGTAATCC 254
99 oProaspProvalansglymetalahtsval1lelyaspi1leglnPheg 116
253 TCCAGATCCTGTGATGGCATGGCAGATGATCAAAAGCATCATTCG 204
116 lYserGlnlelytyrserglyarprolysglytyrarqleuilegylser 132
203 GATCCCAATTAATATCTGTCTTAAGATGATGACATCTGATGCTTCC 154
133 SerSerAlarhCysAlleleSerGlyAsnThrVal1leTyrpaspasly 149
153 TCGCTGCGACATGATCATCTCAGGCAACATGATGGGATTAATA 104
149 sThrProvalCysAspSerGlyLeuLysTyrAlaPheLeuPheLeuPhe 166
103 AACACCTGTTGTGACAGTGAATGAAATATGATTCCTTTCTTTTAC 54
166 rolleHisSerAspPheSerLeuGlu 174
53 CGATACATTCATTAATTTCTCTCGGAA 28
seq_name: gb_est1:A1240881

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seq_documentation_block:
LOCUS A1240881 443 bp mRNA linear EST 28-JAN-1999
DEFINITION g194604.x1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1867134 3'
SIMILAR TO gb:Y00816.cd81 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION A1240881
VERSION A1240881.1 GI:3836278
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 443)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLM at:
www.bio.linn.gov/bbrp/image/image.html
Insert Length: 625 Std Error: 0.00
Seq primer: -40UP from gibco
High quality sequence stop: 373.
Location/Qualifiers
1..443
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1867134"
/clone.lib="NCI CGAP_Kid3"
/lab.host="DH10B"
/note="Organ: Kidney; Vector: pT733D-Pac (Pharmacia) with
a modified polylinker; Site:1: Not 1; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer,"

```

double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT733 vector. RNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.

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BASE COUNT      131 a      80 c      104 g      128 t
ORIGIN
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  Ratio: 5.420      Gaps: 0
  Percent Similarity: 97.872      Percent Identity: 97.163

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alignment\_block:  
US-10-031-904-8 x A1240881/rev ..

Align seg 1/1 to reverse of: A1240881 from: 1 to: 443

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50 rAspAspPheGluPhePro1leGlyThrTyrlleuAsnTyrlGluCysArgp 67
|||||
392 TGATGACTGTGAGTTCCCATGCGACATVTCGAACTATGAAATGCCGCC 343
67 rGlyTyrSerGlyArgProPheSerlelleCysLeuLysAsnSerVal 83
|||||
342 CTGTTATTCCGGAAGACCGTTTCTATCATCTGCTAAATAAACTACATG 293
84 TTPHrSerAlaLysAspLysCysLysArgLysSerCysArgAsnProp 100
|||||
292 TGCAACAGTCTTAAGGACAACTGCAATATCTGTCGTAATCTCC 243
100 oAspProvalansglymetalahtsval1lelyaspi1leglnPheGlys 117
242 ACATCTGTGATGATGACATGACATGATGATCAAAAGCACTCGGAT 193
117 eGln1lelytyrserglyarprolysglytyrarqleuilegylser 133
|||||
192 CCCAATTAATATTTCTGTCTTAAGATGACGATCTGTTGTTCTCG 143
133 SerAlarhCysAlleleSerGlyAsnThrVal1leTyrpaspaslyTh 150
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142 TCTGCCACATCATCATCTCAGGCAACATGTCATTTGGGATTAATAAAC 93
150 rProvalCysAspSerGlyLeuLysTyrAlaPheLeuPheLeuPro 167
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92 ACCTGTTGTGACAGTGAATGAAATATGATCATCTTCTTTTACCGA 43
167 leHisSerAspPheSerLeuGlu 174
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seq\_name: gb\_est1:A1718588

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seq_documentation_block:
LOCUS A1718588 444 bp mRNA linear EST 10-JUN-1999
DEFINITION as4601.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone
IMAGE:2220273 3' similar to gb:Y00816.cd81 COMPLEMENT RECEPTOR TYPE
1 PRECURSOR (HUMAN); mRNA sequence.
ACCESSION A1718588
VERSION A1718588.1 GI:5035844
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 444)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Kitzman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin

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17  oGlyLeuLeuAlaLeuValLeuLeuSerSerPheSerasp 34
163  TGGGTTCCTTGGCGCC. CTGGTTCCTGCTGCTCCCTCCGATC 211
34  lncysanValProglutPleuProPheAlaArgProThrAsnLeuThr 50
212  AATGCAATGTCCCGAATGGCTTCATTCAGGCTACCAAACTACTACT 261
51  AspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGluCysArgpr 67
262  GAGGACTTGGAGTTCCCTTCCGACATCTGACATGACATGCGGCC 311
67  oGlyTyrSerGlyArgProPheSerIleLeuCysLeuLysAsnSerValT 84
312  TGGTTCCTCCGAGACCGCTTTCATCATCTGCTCAAAACCTCACTCT 361
84  rPheSerAlaLysAspLysCysLysArgLysSerCysArgAsnProPro 100
362  GGCACAGTCTAGACACAAAGTCAACCTAATCATCTGCTCACTCCCA 411
101  AspProValAsnGlyMetAla.HisValIleLysAspIleGlnPhe.Gly 116
412  GATCCCTGAATGGCATGGACACATGATCATCAAGACATCCAGTTCAGA 461
117  SerGlnIleLysTyrSerCysProLysGlyTyrArgLeuIleGlySerse 133
462  TCCCAATTAATATCTTGTCTTAAGATACGACTCATTTGGTCTCTC 511
133  rSerAlaThrCysIleIleSerGlyAsnThrValIleTyrAspAsnLysT 150
512  GTCTGC.ACATGCATCATCTCAGGACACATGCTATCTCGGACATCA 560
150  hrProValCys.....AspSerGlyLeuLysTyr 159
561  AAACACCTGTTTGTGGACAGTATGACATCTAC 595
seq_name: gb_est2:BM477528

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## seq\_documentation\_block:

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LOCUS      BM477528          1063 bp      mRNA      linear      EST 05-FEB-2002
DEFINITION AGNCOURT_6484929 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5554371
5', mRNA sequence.
ACCESSION  BM477528
VERSION    BM477528.1 GI:18526570
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 1063)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: egads@remail.nih.gov
            Tissue Procurement: Lou Staudt
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: LHAM2272 row: n column: 04
            High quality sequence stop: 749.
            Location/Qualifiers
                1..1063

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FEATURES
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    /clone="IMAGE:5554371"
    /clone_lib="NIH_MGC_85"
    /tissue_type="lymphoma, cell line"
    /lab_host="DH10B (phage-resistant)"
    /note="Organ: lymph; Vector: pCMV-Sport6; Site_1: NotI;

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Site\_2: Salt: Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.867 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

BASE COUNT 251 a 286 c 272 g 249 t 5 others

## alignment\_scores:

Quality: 649.50 Length: 148  
Ratio: 4.883 Gaps: 2  
Percent Similarity: 89.865 Percent Identity: 81.757

## alignment\_block:

US-10-031-904-8 x BM477528

Align seg 1/1 to: BM477528 from: 1 to: 1063

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    ||| |||: ||| ||| ||| ||| ||| ||| ||| ||| |||
61  CCGGCCCGCGCTCCCTTCCTGCTGCGAGGATCCCTGCGGCTGT 110
24  uValLeuLeu...LeuSerSerPheSerAspGlnCysanValProglut 40
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
111  GGTCTGCTTCCGCTCCCGCTGCGCTGGGGCTCATGCAATGCCCAAT 160
40  rPleuProPheAlaArgProThrAsnLeuThrAspAspPheGluPhePro 56
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
161  GGCTTCATTTGCCAGCGCTACCAACTGATGATGATGATTTGCC 210
57  lIleGlyThrTyrLeuAsnTyrGluCysArgProGlyTyrSerGlyArgpr 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
211  ATGGGACATATCTGACATGATGATGATGATGATGATGATGATG 260
73  oPheSerIleIleCysLeuLysAsnSerValTTrpThrSerAlaLysAsp 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
261  GTTTCTATCATCTGCTTAATAAACTCAGTGTGAGTGGCTTAAGACA 310
90  yScCysLysArgLysSerCysArgAsnProPheAspProValAsnGlyMet 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
311  GGGACAGCATATCAATCATGCTGCTATCTCCAGATCTCGTAATGGCAT 360
107  AlaHisValIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCy 123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361  GTGCATGTATCAAAAGCATCCAGTTCGATCCCAATTAATTTCTTG 410
123  sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIle 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
411  TACTAAGATATACCGACATCATGCTGCTGCTGCCACATGATCATCT 460
140  exGlyAsnThrValIleTyrAspAsnLysThrProValCysAsp 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
461  CAGGTATATCTGCTATTTGGATTAATGAACCTATTTTGTGAC 504
seq_name: gb_est1:A1735459

```

## seq\_documentation\_block:

```

LOCUS      A1735459          356 bp      mRNA      linear      EST 14-JUN-1999
DEFINITION AT1103.X1 Barstead aorta HPLR86 Homo sapiens cDNA clone
IMAGE:2354837 3' similar to gb:Y00816.cdsl COMPLEMENT RECEPTOR TYPE
1 PRECURSOR (HUMAN); mRNA sequence.
ACCESSION  A1735459
VERSION    A1735459.1 GI:5056983
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 356)
            Haller,U., Allen,M., Bowles,L., Dubugre,T., Geisel,G., Jost,S.,
            Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maira,M., Martin
            J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.

```

TITLE Washu-NCI human EST Project  
JOURNAL Unpublished (1997)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu

This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: -40UP from G1bco.

## FEATURES

source

1. 356  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="2354837"  
/clone\_lib="Birstead aorta HPLRB6"  
/sex="male"  
/dev\_stage="adult, age 64"  
/lab\_host="DH10B (phage resistant)"  
/note="Organ: aorta; Vector: pRT3D-Pac (Pharmacia) with a  
modified polylinker; Site.1: EcoRI; Site.2: NotI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACGAACTCTGAAGTGGGACGGCCGCTTTTCTTTTCTTTTCTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
[5' AATTCGGATCGAAC 3' and 5' GTTGGATCGG 3'], digested  
with Not I and cloned into the Not I and Eco RI sites of  
the modified pRT3 vector. Library constructed by Bob  
Birstead."

BASE COUNT 107 a 61 c 77 g 111 t  
ORIGIN

alignment\_scores:  
Quality: 603.00 Length: 114  
Ratio: 5.432 Gaps: 0  
Percent Similarity: 97.368 Percent Identity: 97.368

alignment\_block:  
US-10-031-904-8 x AT735459/rev ..

Align seg 1/1 to reverse of: AT735459 from: 1 to: 356

```

61 LeuAsnTyGluCysArgProGlyTyrSerGlyArgProPheSerIleI 77
|||||
355 CTGAAGTATGAAATGCCGCCCTGTATTCGGAAGACCGTTTCTATCAT 306
77 eCysIleuLysAsnSerValTrrPThrSerAlaLysAspLysCysIle 94
|||||
305 CTCCCTAAATAAACTCAGTCTGACAGAGCTCAAGGACAGTGAACGTA 256
94 ySercYsaTgaAnpProApsProValaAnGlyMeLAlaHsValIle 110
|||||
255 AATCATGTCGTAACTCCATCCTCGAATGCGATGACATGATGATC 206
111 LysAspIleGlnPheGlySerGlnIleLysTyrSerCysProLysGly 127
|||||
205 AAAGACATCCAGTTCAGATCCCAAAATTAATATTTCTTCTTAAGATA 156
127 rArgLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAsnThrv 144
|||||
155 CCGACTCATATTGGTTCTCGTCCACACATGATCATCTCAGGCAACCTG 106
144 alIeTrpAspAsnLysThrProValCysAspSerGluLeuLysTyrAla 160
105 TCATTGGGATATATAAACCTGTTTGGACAGAGACTTGAATATATGCA 56
161 PheLeuPheLeuLeuProIleHisSerAsnPheserLeuGlu 174
|||||
55 TTCCTATTCTCTAAAGATACATCTTAATTTTCTCTGAA 14

```

seq\_name: gb\_est2:766824

seq\_documentation\_block:

LOCUS T66824 346 bp mRNA linear EST 07-MAR-1995  
DEFINITION ya50b08.r3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
IMAGE:66327 5' similar to gb:y00816\_cds1 COMPLEMENT RECEPTOR TYPE 1  
PRECURSOR (HUMAN); mRNA sequence.

ACCESSION T66824  
VERSION T66824.1 GI:676264  
KEYWORDS EST

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 346)  
Hillier, L., Clark, N., Dubuque, T., Elliston, R., Hawkins, M., Holman,  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston,  
R., Williamson, A., Wohlmann, P. and Wilson, R.

AUTHORS

TITLE The Washu-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Other\_ESTs: ya50b08.s3.exp

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
High quality sequence stops: 324  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: T7  
High quality sequence stop: 324.

## FEATURES

source

Location/Qualifiers

1. 346  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="66327"  
/clone\_lib="Soares fetal liver spleen INFLS"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia)  
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI;  
1st strand cDNA was primed with a Pac I - oligo(dT) primer  
[5' AACTGGAATTAATTAAGATCTTTTCTTTTCTTTTCTTTTCTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified pRT3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 67 a 101 c 77 g 97 t 4 others  
ORIGIN

alignment\_scores:  
Quality: 555.00 Length: 108  
Ratio: 5.236 Gaps: 2  
Percent Similarity: 98.148 Percent Identity: 97.222

alignment\_block:  
US-10-031-904-8 x T66824 ..

Align seg 1/1 to: T66824 from: 1 to: 346

```

4 ProValArgLeuGluArgProPheProSerArgArgPheProGlyLeuLe 20
|||||
24 CCGCTCCCTCTCGAGCGCTCCCTTCCCGCGCGCTTCCGCGGTTCTCT 73
20 uLeuAlaIleuValLeuLeuLeuSerSerPheSerArgPheGlnCysAsn 37
|||||
74 TCTGCGCGCCCTGCTGTGCTGCTCTCTCTCTCGATCATGCAATG 123
37 aProGluTrpLeuProPheAlaArgProThrAsnLeuThrAspPhe 53

```



IMAGE Consortium ([image.jnl.gov](http://image.jnl.gov)) for further information  
Insert Length: 791 Std Error: 0.00  
Seq primer: M13Rpl  
High quality sequence stop: 300.  
Location: 0.0141414

## FEATURES

1.541

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/organism="Homo sapiens"
/db_xref="GDB:466397"
/db_xref="taxon:9606"
/clone="IMAGE:110780"
/clone_lib="Scars fetal liver spleen INFLS"
/sex="male"

```

BASE COUNT	122 a	121 c	110 g	178 t	10 others
ORIGIN					

[illegible]

alignment\_block:  
US-10-031-904-8 x T83269

Align seg 1/1 to: T83269 from: 1 to: 541

16 PheProGlyLeuLeuLeuAlaAlaLeuValLeuLeuLeuSerSerPhe 32  
5 TTTCCTGGGTTGCTTCGGGGCCCTGGTGTGTGCTCTCTCTCTCTC 54  
32 AspGlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnL 49  
55 CGATCAATGCAATGCTCCGGAAAGGCTTCAATGGCAAGCCCTACCAAC 104  
49 euThrAspAspPheGluPheProIleGlyThrTyrLeuAsnTyrGlnCys 65  
105 TTAACGATGACTTGGAGTTCCCATGGCAATATGTGAACTAGTAATGC 154  
66 ArgProGlyTyrSerGlyArgProPheSerIleGlyLeuLysAsnSe 82  
155 CGCCCTGGTATTTCGGAAAGACGTTTCTATCATCTGCTCTAAAAACTC 204  
82 ValTrpThrSerAlaLysAspLysCysLysArgLysSerCysArgAsn 98  
205 AGCTGAGCAAGTCTTAAGCAACAATGGTAACGTAAACGTAAATCATGTCTGAT 254  
99 ProProAspProValAsnGlyMetAlaHisValIleLysAspIleG 114  
255 CCTCCAGATCCTGGAATGGGATGGCAACATGTGGATTAAAGACATCCA 304  
114 nPheGly...SerGlnIleLysTyrSerCysProLysGly...Tyr 127  
127 TTTT...TT 180  
305 GTTTCGGATTCCCAAAATTAAATTAATTTCTTGTCTCTAAAGGATACCGANT 354  
128 ArgLeuIleGlySerSerSerAlaThrCysIleIleSerGlyLysThrVal 144  
144 TTTT...TT 198  
355 CATGGGTTTCTGTGTTGGCCACATGCAATGCATCTCTTTCAGGGCAACATG 404  
144 IleIleTrpAspAsn...LysThrProValCys...AspS 155  
405 TTTCATTGGGGGGTATTATAAAACCCGCTTTTGTGTGGACAGTNGAGTTTG 454

```

155 ergIleuLysTyrAlaIleuLeuProIle.HisSerAsp 171
    :: :: :: || || ||||| ||| ||
455 GAANTATGCGNTCCCATTTTCCTT..TTACNATATCAITTTATTT 501

```

```

171 eserLeu 173
      1:::111
502 TTTNCTC 508

```

seq\_name: gb\_est2:H73873

```
seq_documentation_block:
  docnum: 173873
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DEFINITION  
ys14d08.r1 s  
TWCE-214767

1 PRECURSOR  
H73973

```
VERSION H73873.1  GI
KEYWORDS EST
```

SOURCE	human.
ORGANISM	Homo sapiens

Eukaryota; Mammalia; E

REFERENCE	1 (bases 1
AUTHORS	Hillier/L.

CRISOE, S.,  
, M., Hultmar

P.B., MOLLIS,  
Schellenberg

**TITLE** Generation 2

**MEDLINE** 97044478

Washington

Tel: 314 286

Email: [est@...](mailto:est@...)

High quality

This clone is

Insert Length

High quality

1. source

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/cj

 $\frac{1}{\delta \epsilon}$ /nc  
with

151

doi:10.1017/S0007122614000091

and wet

BASE COUNT	83 a
------------	------

ORIGIN

alignment scores:

Quality: 4  
Ratio: 4

Percent similarity: 94

```

Email: est@watson.wustl.edu
Insert Size: 706
High quality sequence stops: 275
Source: IMAGE Consortium, LINT
This clone is available royalty-free through LINT ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 706      Std Error: 0.00
Seq primer: M13Rp1
High quality sequence stop: 275.
Location/Qualifiers
    1. .440
       /organism="Homo sapiens"
       /db_xref="taxon:9606"
       /clone_1b="IMAGE:214767"
       /clone_1b="Soares fetal liver spleen INFLS"
       /sex="male"
       /dev_stage="20 week-post conception fetus"
       /lab_host="PH10B (ampicillin resistant)"
       /note="Organ: Liver and Spleen; Vector: pRTT3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
15' AACTGAGAGATTATTAAGATCGTTTTTTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pRTT3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT      83 a      128 c      100 g      125 t      4 others
ORIGIN
alignment_scores:      Quality:      497.00      Length:      118
Ratio:      4.560      Gaps:      7
Percent Similarity:      92.373      Percent Identity:      88.983

```

alignment\_block:  
US-10-031-904-8 x H73873 ..

Align seg 1/1 to: H73873 from: 1 to: 440

```

4 ProValArgLeuGluArgProPheProSerArgArgPheProGlyLeu 20
93 CCGCTCCGCTCGAGGCTCCCTTCCCTCCGCGGCTTCTGGTTCCT 142
20 ULeuAlaLeuValLeuLeuLeuSerSerPheSerAspGlnCysAsn 37
143 TCTGGCGGCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 192
37 alProGluTrpLeuProPheAlaArgProThrAsnLeuThrAspAsp 53
193 TCCCGGAATGGCTTCCATTTGCCAGGCTTACCACTGATGACTTT 242
54 GluPheProIleGlyThrTyrLeuAspTyrGlnCysArgPro GlyTyr 70
243 GAGTTTCCCTTGGACATATCTGAACATATCAATCCGCTGGTATTT 292
70 erGlyArgProPheSerIleIleCysLeuLysAsnSerValTrp Thr 86
293 CCGGAACCCGCTTCTATCATCTCCCTTAACTAGCTGGACAAAG 342
86 fAlaLysAspLysCysLysArg.LysSerCys.ArgAsnPro.ProAsp 102
343 TGCCTAAGACAAAGTCAACGTTAATCATGTCTGTAATCTTCCAGATC 392
102 roValAsn.GlyMetAlaHisValIle.....LysAspIle 113
393 CTGTGATTTGGCATTTGGCATTTGTGATCAAAAGACATT 434
seq_name: gb_est1:AA212152

```

seq\_documentation\_block:

LOCUS AA212152 601 bp mRNA linear EST 31-JAN-1997  
DEFINITION Mus musculus melanoma (#937312) Mus musculus CDNA  
clone IMAGE:651900 5', similar to gb:M23529 Mus musculus complement  
receptor (MOUSE);, mRNA sequence.

ACCESSION AA212152  
VERSION AA212152.1 GI:1810867

KEYWORDS

SOURCE

ORGANISM

REFERENCE

UTTERS

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/tissue\_type="melanoma"  
/dev\_stage="M2 cells"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: skin; Vector: pBluescript SK-; Site: 1: EcoRI  
; Site: 2: XhoI; Cloned unidirectionally. Primer: oligo  
dT. From M2 cells, a highly metastatic derivative of the  
Uni-ZAP XR Vector, -5' adaptor sequence: 5' GAATTCGCGCAGAG  
3' -3' adaptor sequence: 3' CTCGAGTTTCTTTTCTTTT 3'

BASE COUNT 149 a 137 c 140 g 175 t  
ORIGIN

alignment\_scores:  
Quality: 420.50 Length: 143  
Ratio: 3.754 Gaps: 1  
Percent Similarity: 78.322 Percent Identity: 55.245

alignment\_block:

US-10-031-904-8 x AA212152 ..

Align seg 1/1 to: AA212152 from: 1 to: 601

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13 SerArgArgPheProGlyLeuLeuAlaLeuValLeuLeuLeu 29
69 AGCCTTGGCGGAGAGAGTCAAGCTAGAACTTTGGCTGCTTCTTCT 118
29 rSerPheSer..AspGlnCysAsnValProGluTrpLeuProPheAla 45
119 GCCATTTACTTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 168
45 rGProThrAsnLeuThrAspAspPheGluPheProIleGlyThrTyr 61
169 AACCTATAAATCTAATCTGATGATCATCTTCCCATTTGGAAACATAT 218
62 AsnTyrGlnCysArgProGlyTyrSerGlyArgProPheSerIleLeu 78
219 TTGTATTAATGTCTCCAGATATATCAAGAGCAGTCTCTATCACCTG 268
78 sLeuLysAsnSerValTrpThrSerAlaLysAspLysCysLysArg 95
269 CAAACAAAGACTCAACCTGACGACGAGTCAAGATTAATGCGAAGAC 318
95 erCysArgAsnProPheProValAsnGlyMetAlaHisValIleLys 111
319 AATGTAATAACTCTTCAGATCTGAGATGCTTGTGATGACACACA 368
112 AspIleGlnPheGlySerGlnIleLysTyrSerCysProLysGlyTyr 128
369 GGCATTAGTTTGATCCCGTATTAATTAATCTTGTATCAAGATACCG 418
128 gLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAsnThrVal 145
419 CCTCATTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 468
145 letPaspAsnLysThrProValCysAsp 154
469 ATTGGGATCTAGAGCAGCCCATTTGTGAG 497
seq_name: gb_est2:BG077250

```

seq\_documentation\_block:

LOCUS BG077250 577 bp mRNA linear EST 26-JAN-2001  
DEFINITION H3013A12-5' N1A Mouse 15K cDNA Clone Set Mus musculus CDNA clone  
H3013A12 5', mRNA sequence.

ACCESSION BG077250  
VERSION BG077250.1 GI:12559818

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 577)













140 erglyAsnThrValIleTrpAspAsnLysThrProValCysasp 154  
 |||:::|||||:::|||||:::|||||:::|||||  
 470 CAGGTGATGATGTCATTTGGATATGAAACACCTATTGTGTGAC 513

seq\_name: /cgn2\_6/prodata/2/lna/backfile1.seq:5472939-1

seq\_documentation\_block:  
 ; Patent No. 5472939  
 ; APPLICANT: FEARON, DOUGLAS T.; KLUCKSTEIN, LLOYD B.; WONG,  
 ; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
 ; H.; MARRIDES, SAVVAS; MARSH, HENRY C. JR.  
 ; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT  
 ; MEDIATED DISORDERS  
 ; NUMBER OF SEQUENCES: 30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/138,825  
 ; FILING DATE: 19-OCT-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 568,128  
 ; FILING DATE: 24-SEP-1990  
 ; APPLICATION NUMBER: 412,745  
 ; FILING DATE: 26-SEP-1989  
 ; APPLICATION NUMBER: 332,865  
 ; FILING DATE: 03-APR-1989  
 ; APPLICATION NUMBER: 176,532  
 ; FILING DATE: 01-APR-1988  
 ; SEQ ID NO: 1:  
 ; LENGTH: 6951  
 5472939-1

alignment\_scores:  
 Quality: 649.50 Length: 148  
 Ratio: 4.883 Gaps: 2  
 Percent Similarity: 89.865 Percent Identity: 81.757

alignment\_block:  
 US-10-031-904-8 x 5472939-1 ..

Align seg 1/1 to: 5472939-1 from: 1 to: 6951

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10 ProPheProSerArgArgPhe.....ProGlyLeuLeuLeuAlaLe 24
||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 CCGGGCGCGGCTCCCTCTGCTGGGAGAGATCCCTGCTGGCGGTGT 119
24 uValLeuLeu...LeuSerSerPheSerAspGlnCysAsnValProGluT 40
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 GGTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 169
40 rPLeuProPheAlaArgProThrAsnLeuThrAspAppheGluPhePro 56
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
170 GGCCTTCATTTGCCAGGCTACCACTAAGTATGATGTTGAGTTTCC 219
57 lIleGlyThrTyLeuAsnTyrgLysArgProGlyTyrSerGlyArgPr 73
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
220 ATTGGGACATATCTGAATGATGATGCGGCTGTTATTCGGGAAGCC 269
73 oPheSerIleIleCysLeuLysAsnSerValTrpThrSerAlaLysAspL 90
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
270 GTTTTCTATCATCTGCTAAATAAAGTCTGAGTGGTGTGAAGGACA 319
90 yScyLysArgLysSerCysArgAsnProPheAspProValAsnGlyMet 106
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
320 GGTGAGACGTAAATCATGTGTAATCTTCACATCTGTGAATGCGCATG 369
107 AlaHisIleLysAspIleGlnPheGlySerGlnIleLysTyrSerCyl 123
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
370 GTGATGTGATCAAGGATCCAGTTCGATGCCAATTAATATTTCTTG 419
123 sProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleLys 140
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
420 TACTAAAGATACCGACTCATGTCTCTGCTGCTGCCACATCATCATCT 469

```

140 erglyAsnThrValIleTrpAspAsnLysThrProValCysasp 154  
 |||:::|||||:::|||||:::|||||:::|||||  
 470 CAGGTGATGATGTCATTTGGATATGAAACACCTATTGTGTGAC 513

seq\_name: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:US-08-769-967A-33

seq\_documentation\_block:  
 ; Sequence 33, Application US/08769967A  
 ; Patent No. 5859223  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mossakowska, Danuta E.I.  
 ; APPLICANT: Smith, Richard A.G.  
 ; APPLICANT: Dodd, Ian  
 ; TITLE OF INVENTION: Soluble CRI Derivatives  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
 ; STREET: P.O. Box 1539  
 ; CITY: King of Prussia  
 ; STATE: Pennsylvania  
 ; COUNTRY: USA  
 ; ZIP: 19406  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/769,967A  
 ; FILING DATE:  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/440,569  
 ; FILING DATE: 15-May-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: King, William T.  
 ; REGISTRATION NUMBER: 30,954  
 ; REFERENCE/DOCKET NUMBER: P30423C2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (610) 270-5364  
 ; TELEFAX: (610) 270-5090  
 ; INFORMATION FOR SEQ ID NO: 33:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 605 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-08-769-967A-33

alignment\_scores:  
 Quality: 635.00 Length: 121  
 Ratio: 5.336 Gaps: 0  
 Percent Similarity: 98.347 Percent Identity: 90.909

alignment\_block:  
 US-10-031-904-8 x US-08-769-967A-33 ..

Align seg 1/1 to: US-08-769-967A-33 from: 1 to: 605

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34 GlnCysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuTh 50
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7 CAGTGCAACGCTCCGGAATGCTGCGGCTGCGGCGCGCACCAACCTGAC 56
50 rAspAspPheGluPheProIleGlyThrTyLeuAsnTyrgLysArgP 67
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
57 TGATGAATTTAGTTCGCCGATCGGTACTGACCTGAACTGCAATGCCGCC 106
67 rGlyTyrSerGlyArgProPheSerIleIleCysLeuLysAsnSerVal 83
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```



```

111 yaspilleginphesylserglnleleystyrsercysprolysglytyr 127
|||||
2911 CAGTTCACAGCTTGGATCAACGTTATATCTGTATATGAGGTTT 2960
128 ArgLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAsnThrVal 144
|||||
2961 CGACTCATCTGTTCCCATCTACTACTGTCTCTGTCAGCAATATATGT 3010
144 lIleTrpAspAsnLysThrProValCysAsp 154
|||||
3011 CACATGGGATPAGAGGACCACTTATGTGAG 3041

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seq\_name: /cgn2\_6/ptodata/2/1na/6B\_COMB.seq:us-08-139-195-1

seq\_documentation\_block:

; Sequence 1, Application US/08139195

; Patent No. 6218520

; GENERAL INFORMATION:

APPLICANT: Atkinson, John P.

TITLE OF INVENTION: RECOMBINANTLY PRODUCED HUMAN MEMBRANE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst

STREET: 1100 Peachtree Street, Suite 2800

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30309-4530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/139,195

FILING DATE: 20-OCT-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/948,350

FILING DATE: 21-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/384,210

FILING DATE: 21-JUL-1989

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: WU100CON

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)-815-6508

TELEFAX: (404)-815-6555

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1545 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Human t-Cell Line HSB2

US-08-139-195-1

alignment\_scores:

Quality: 291.00

Ratio: 2.853

Percent Similarity: 60.714

Length: 168

Gaps: 6

Percent Identity: 40.476

alignment\_block:

US-10-031-904-8 x US-08-139-195-1

Align seq 1/1 to: US-08-139-195-1 from: 1 to: 1545

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1 MetAlaProProValArgLeuGluArgProPheProSerArgAlaPhePr 17
|||||
44 ATGAGCCTCCCGCCGCCGCGAGTGTCCTTCCCTCCGCGCTTCC 93
17 ogLLeuLeuAlaAlaValLeuLeuLeuSerPheSerAspG 34
|||||
94 TGGGTGCTTCTGCGCGCATGTGTGCTGTACTCTCTCCGATG 143
34 lncysasnValProGluTrpLeuProPhe.....Ala 44
|||||
144 CCTGTAGGAGCCCA.....CCATTGGAAGCTATGAGCTCATTTGGT 187
45 ArgProThrAsnLeuThrAspPheGluPheProIleGlyThrTyrLe 61
|||||
188 AATCCAAACCCCTAC.....TATGAGATTGGTGAACGAGT 222
61 uasnTyrgLcysArgProGlyTyrSerGlyArgPro.....PheS 75
|||||
223 AGATTATAGTGTAAAAAGATACTCTATATACCTCTCTGCGACCC 272
75 erllelecyLeuLysAsnSerValTrpThrSer..AlaLysAspLys 90
|||||
273 ATACTATTCTTGATCGGATCATACATGCTACGCTCGTCAGATACGCC 322
91 CysLysArgLysSerCysArgAsnProProAspProValAsnGlyMetAl 107
|||||
323 TGTTATAGAGAAACATGTCATATATACGAGATCCTTAAAGGCCAAG 372
107 ahLsValIleLys...AspIleGlnPheGlySerGlnIleLysTyrSerC 123
|||||
373 AGTCCCTGCATGAAATGAGACTTACGAGTTTGTTATACAGATGACCTTATT 422
123 yspProLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIle 139
|||||
423 GTAATGAGGGTATTACTTAATTGGTGAAGAAATCTATATGTGAACCTT 472
140 SerGlyAsnThrValIleTrpAspAsnLysThrProValCysAspSerG 156
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473 AATGATCAGTACATTTGAGACGGTAAAGCCCAATATATGAAAGGT 522
156 uLeu 157
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523 TTG 526

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seq\_name: /cgn2\_6/ptodata/2/1na/5A\_COMB.seq:us-08-310-416A-11

seq\_documentation\_block:

; Sequence 11, Application US/08310416A

; Patent No. 5679546

; GENERAL INFORMATION:

APPLICANT: Jone-Long Ko et al.

TITLE OF INVENTION: CHIMERIC PROTEINS WHICH BLOCK

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/310,416A

FILING DATE: 22-SEP-1994

CLASSIFICATION: 435



## ATTORNEY/AGENT INFORMATION:

NAME: Paul T. Clark  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 06180/005001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154

## INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 903 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-310-416A-11

## Alignment scores:

Quality: 289.00 Length: 173  
 Ratio: 2.890 Gaps: 6  
 Percent Similarity: 57.803 Percent Identity: 39.884

## alignment\_block:

US-10-031-904-8 x US-08-310-416A-11 ..

Align seg 1/1 to: US-08-310-416A-11 from: 1 to: 903

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1  MetAlaProValArgLeuGluArgProPheProSerArgArgPhePr 17
4  ATGGAGCCTCCCGCGCGCGGAGTGCCTTCTTCTTCTTCCGCGCTTCC 53
17  oGlyLeuLeuAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
54  TGGGTTGCTTCTGGCGGCGCATGTGCTCTGCTGCTCTTCCGATG 103
34  IncysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
104  CCTGTGAGAGCA.....CCACA..... 123
51  AspaSpPheGlu.....PhePr 56
124  ....TTTGAAGCTATGAGCTCATTTGTAAACCAAAACCTACTATAGA 167
56  oLleGlyThrTrLeuAsnTrpGluCysArgProGlyTrpSerGlyArgP 73
168  GATGTGTAACGATGATATATAGTAAAGATACTTCTATATAG 217
73  ro.....PheSerLeuLeuGlyLeuAsnSerValTrpThrSer 86
218  GTTCCTTCCACCCATCTATTGTGATCGAATCATACATGCGCTACT 267
87  ...AlaLysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
268  GTCTCGATGAGCGCTGTATAGAGAAACATGTCATATAGCGGATCC 317
102  oValAsnGlyMetAlaHisValIleLys...AspLleGlnPheGlySerG 118
318  TTTAAATGGCCAGACGCTCCCAATGGACCTTAGCGATTGGTTATC 367
118  InleLysTrpSerCysProLysGlyTrpArgLeuIleGlySerSerSer 134
368  AGATGACACTTATTTGTATGAGGTTATTTACTTATTTGTTAGAAAT 417
135  AlaThrCysIleLleSerGlyAsnThrValIleTPAspAsnLysThrPr 151
418  CTATATTGGAACTTAAGATCAGTAGCAATTGGAGCGGTAAGCCGCC 467
151  oValCysAspSerGluLeu 157
468  AATATGTGAAAAGTTTTC 486

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seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-888-171-11

## seq\_documentation\_block:

Sequence 11, Application US/08888171

Patent No. 5851528

GENERAL INFORMATION:

APPLICANT: Jone-Long, Ko

APPLICANT: Higgins, Paul J.

APPLICANT: Yeh, C. Grace

TITLE OF INVENTION: METHODS OF INHIBITING COMPLEMENT

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson, P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/888,171

FILING DATE: 03-JUL-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/310,416

FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-507

TELEFAX: 617/542-890

TELEX: 200154

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 903 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-888-171-11

## alignment\_scores:

Quality: 289.00 Length: 173  
 Ratio: 2.890 Gaps: 6  
 Percent Similarity: 57.803 Percent Identity: 39.884

## alignment\_block:

US-10-031-904-8 x US-08-888-171-11 ..

Align seg 1/1 to: US-08-888-171-11 from: 1 to: 903

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1  MetAlaProValArgLeuGluArgProPheProSerArgArgPhePr 17
4  ATGGAGCCTCCCGCGCGCGGAGTGCCTTCTTCTTCTTCCGCGCTTCC 53
17  oGlyLeuLeuAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
54  TGGGTTGCTTCTGGCGGCGCATGTGCTCTGCTGCTCTTCCGATG 103
34  IncysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
104  CCTGTGAGAGCA.....CCACA..... 123
51  AspaSpPheGlu.....PhePr 56
124  ....TTTGAAGCTATGAGCTCATTTGTAAACCAAAACCTACTATAGA 167

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56 oiiiegllfhyrthylrleasrtyglucysargproliyltyrserscilyarnp 73
    ||||| .....|||:||||:| |||||
168 gattggtgaaacagcagtrtgattatatactgrraaaagaaagatccttcatatfac 217
    73 ro.....pheserillecysleuylsasnservaltrprrhsr 86
    || .....||| ||||| .....|||
218 ctccctctgcacaccattactatttcttgatnctggaatcattacnaccgtacct 267
    87 ..Alalysasplyscysilsystrglyserscysatrgasnpropioaspr 102
    :::: ||| ||| ||| .....|||
268 gtctcgaagacagccctgttatgagaaacatgctcatatatnaccggatcc 317
    102 ovalasnglymetalaahlsvalillelys...asplileglnpheglsyerg 118
    ||:|||||:|||||
318 tttraaatggcccaacgacgtccctccgcaaatggcagcttaccagatttggtatc 367
    118 lnilleltyrseryscysprolysglytyrargleuileglserserser 134
    ||:::ctt: ||| .....||| |||||:||||:
368 agatgcaccttattttatnagagggttatnactttatnaggcgaaaat 417
    135 alatrhcyslilellesercllysanthrvaliletrpaspasnlyshnpr 151
    ||| .....|||:||||:|||||:||||| ||
418 ctatattgtgcacactrraaagacacagtagcaaatnaggaccggttaagcccc 467
    151 ovalysaspserscyluu 157
    ||:|||||:|||||
468 aaatratggaanaacgttttg 486

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seq\_name: /cgn2\_6/ptodata/2/1na/6A\_COMB.seq:US-08-793-418-1

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seq.documentation block:
Sequence 1, Application US/08793,418C
Patent No. 6130062
GENERAL INFORMATION:
APPLICANT: The Austin Research Institute
TITLE OF INVENTION: Improvements in Production of Proteins in Host Cells
FILE REFERENCE: CALA-100
CURRENT APPLICATION NUMBER: US/08/793,418C
CURRENT FILING DATE: 1997-02-25
EARLIER APPLICATION NUMBER: PCT/AU95/00553
EARLIER FILING DATE: 1994-08-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1134
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CD46 cDNA
US-08-793-418-1

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[illegible]

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alignment_block:
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Align seg 1/1 to: US-08-793-418-1 from: 1 to: 1134

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1  Metal1ProteinValArgLeuGluArgProPheProSerArgArgPhePr 17
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1  ATGAGAGCTTCCGCGCGCGCGAGTGTCTTCTCTCTCGCGCGTTCC 50
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
17  oglyLeuLeuLeuAlaLeuValLeuLeuLeuSerSerPheSerAspG 34
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
51  TGGGTGCTTCTGGCGGCGCATGTGTGTCTGTCTCTCTCCGATG 100
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
34  lncysanValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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101 CCTGTGAGGAGCCA.....CCACA..... 120
102
51 AspAspPheGlu.....PhePr 56
121 .....TTTGAAGCTATGAGACTCATTTGGTAAACCAAAACCTCTACTATGA 154
122
56 oligGlyThrTYrLeuAsnTYrGluCysArgProGlyTyrSerGlyArgP 73
123 |||||
165 GANTGGTGAACGAGATGATTAATGACTATTAAGATTAATAAAAGAACTCTTATATAC 214
166
73 ro.....PheSerIleIleGlyCysLeuIysAsnSerValIleTrpHisSer 86
167 |||||
215 CTCCTCTGTCGCCACCCATACACTATATTTGTATCGCAATCATACATGCGTACT 264
216
87 ...AlaIysAspIleCysIysArgIysSerCysArgAsnProPheAspPr 1020
217 ::: |||||
265 GCTCTCAGATGACGCCCTGTTATATGAAACAAACATGTCATATATATACGGATCC 3144
266
102 oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
267 |||||
315 TTTAAATATGGCCAAACGACGTCCTCGCAAAAGGGACACTTACAGATTTGGTTATC 3644
316
118 IlnIleIysTYrSerCysPProIysGlyTYrArgIleuIleGlySerSerSer 134
317 ||::: |||
365 AGATGCACCTTATATTTGTAATGAGGGTTTATCTTATATTTGGTGAAGAAATT 4144
366
135 AlaThrCysIleIleSerGlyIysAsnThrValIleTrpAspAsnIysTrpPr 151
367 |||||
415 CTATATTTGGTGAACCTTAAAGATCATCTACCAATTTGGAGCGGTAAAGCCCCC 4644
416
151 oValIysAspSerGluLeu 157
417 ::::|
465 AATATGTGAAGAGCTTTTG 483

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465 AATATCTGAAAGGTTTG 483

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seq_name: /cgm2_6/prodata/2/lna/6A_COMB.seq:US-08-793-418-3
seq_documentation_block:
? Sequence 3, Application US/08793418C
? Patent No. 6130062
? GENERAL INFORMATION:
? APPLICANT: The Austlin Research Institute
? TITLE OF INVENTION: Improvements in Production of Proteins in Host Cells
? FILE REFERENCE: CALA-100
? CURRENT APPLICATION NUMBER: US/08/793,418C
? CURRENT FILING DATE: 1997-02-25
? EARLIER APPLICATION NUMBER: PCT/AU95/00553
? EARLIER FILING DATE: 1994-08-30
? NUMBER OF SEQ ID NOS: 15
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 1134
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: CD46 cDNA
? OTHER INFORMATION: subscr3 variant
US-08-793-418-3

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alignment\_scores:

Quality:	289.00	Length:	173
Ratio:	2.890	Gaps:	6
Percent Similarity:	57.803	Percent Identity:	39.888

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alignment_block:

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Align seg 1/1 to: US-08-793-418-3 from: 1 to: 1134

1 MetalapProValArgLeuGluArgProPheProSerArgArgPhePr 17  
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 1 ATGAGACCTCCCGCGCGCGGAGTGTCCCTTCTTCCTGGGCGCTTCC 50

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17  oGlyLeuLeuAlaAlaLeuValLeuLeuSerSerPheSerAspG 34
   |||||||
51  TGGGTTCCTTGGCGCGCATGGTTCCTGCTGACTCTTCCCATG 100
   |||
34  IncysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
   |||
101 CCTGTGAGGAGCCA.....CCACA..... 120
   |||
51 AspAspPheGlu.....PhePr 56
   |||
121 .....TTTGAAGCTATGAGCTATTGTGTAACCAAAACCTACTATGA 164
   |||
56  oIlleGlyThrTyLeuAsnTyGluCysArgProGlyTyrSerGlyArgP 73
   |||
165 GATTGGTGAACGAGTATGATTAAGTATTAAGTATTAAGTATTAAGTATTA 214
   |||
73  ro.....PheSerIleLeuGlySerLeuYsAsnSerValTrpThrSer 86
   |||
215 CTCCTCTTCCACCCATCTACTATTGTGATCGGAATCATATACATGGCTACT 264
   |||
87  ...AlaIysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
   |||
265 GCTGTGAGTACGCGCTGTATATGAGAACAATGTCATATATACGGATAC 314
   |||
102 oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
   |||
315 TTTAAATGGCCAGACGCTCCGCAAAATGGACCTTACGAGTTGGTATAC 364
   |||
118 InileLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSer 134
   |||
365 AGATGCACTTATTGTATGATGAGGCTTATTACTTAAATGGTGAAGAAT 414
   |||
135 AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151
   |||
415 CTTATATTGAACTTAAAGATCACTAGCAATTTGGAGCGGTAAAGCCGCC 464
   |||
151 oValCysAspSerGluLeu 157
   |||
465 AATATGTGAAGAAGTTTGG 483

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seq\_name: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:US-08-528-057-41

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seq_documentation_block:
; Sequence 41, Application US/08528057
; Patent No. 5846715
; GENERAL INFORMATION:
; APPLICANT: PURCELL, Damian F. J.
; APPLICANT: MCKENZIE, Ian F. C.
; TITLE OF INVENTION: CD46 VARIANTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/528,057
; FILING DATE: CONCURRENTLY HEREMITH
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/961,686
; FILING DATE: 11-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU91/00199
; FILING DATE: 10-MAY-1991
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: AU PK0133/90
; FILING DATE: 11-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 17227/112 DACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1247 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 83..1192
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 185..1192
; US-08-528-057-41

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alignment_scores:
Quality: 289.00 Length: 173
Ratio: 2.890 Gaps: 6
Percent Similarity: 57.803 Percent Identity: 39.884

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alignment\_block:  
US-10-031-904-8 x US-08-528-057-41 ..

Align seg 1/1 to: US-08-528-057-41 from: 1 to: 1247

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1  MetaLapProValArgLeuGluArgProPheProSerArgArgPhePr 17
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83  ATGAGCCTCCCGCGCGCGAGTGTGCTTCTTCTGCGGCTTTC 132
   |||
17  oGlyLeuLeuAlaAlaLeuValLeuLeuSerSerPheSerAspG 34
   |||
133 TGGTTCCTTCTGCGCGCGAGTGTGCTTCTTCTGCGGCTTTC 182
   |||
34  IncysAsnValProGluTrpLeuProPheAlaArgProThrAsnLeuThr 50
   |||
183 CCTGTGAGGAGCCA.....CCACA..... 202
   |||
51 AspAspPheGlu.....PhePr 56
   |||
203 .....TTTGAAGCTATGAGCTCATTTGTGTAACCAAAACCTACTATGA 246
   |||
56  oIlleGlyThrTyLeuAsnTyGluCysArgProGlyTyrSerGlyArgP 73
   |||
247 GATTGTGTAACGAGTATGATTAAGTATTAAGTATTAAGTATTAAGTATTA 296
   |||
73  ro.....PheSerIleLeuGlySerLeuYsAsnSerValTrpThrSer 86
   |||
297 CTCCTCTTCCACCCATCTACTATTGTGATCGGAATCATATACATGCGTACT 346
   |||
87  ...AlaIysAspLysCysLysArgLysSerCysArgAsnProProAspPr 102
   |||
347 GCTGTGAGTACGCGCTGTATATGAGAACAATGTCATATATACGGATAC 396
   |||
102 oValAsnGlyMetAlaHisValIleLys...AspIleGlnPheGlySerG 118
   |||
397 TTTAAATGGCCAGACGCTCCGCAAAATGGACTTACGAGTTGGTATAC 446
   |||
118 InileLysTyrSerCysProLysGlyTyrArgLeuIleGlySerSerSer 134
   |||
447 ACATGCACTTATTGTATGAGGAGTATTAAGTATTAAGTATTAAGTATTA 496
   |||
135 AlaThrCysIleIleSerGlyAsnThrValIleTrpAspAsnLysThrPr 151

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497 CTATATGTGAACTTAAGATCAGTAGCAATTGTGAGCGGTAAAGCCCC 546

151 oValcysAspSerGluLeu 157

547 AATATGTGAAAAGGTTTGG 565

seq\_name: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq:US-08-528-057-45

seq\_documentation\_block:

Sequence 45 Application US/08528057

Patent No. 5846715

GENERAL INFORMATION:

APPLICANT: PURCELL, Damian F. J.

APPLICANT: MCKENZIE, Ian F. C.

TITLE OF INVENTION: CDA6 VARIANTS

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/528,057

FILING DATE: CONCURRENTLY HEREWITH

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/961,686

FILING DATE: 11-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU91/00199

FILING DATE: 10-MAY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P0133/90

FILING DATE: 11-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 17227/112 DACO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 1304 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 94..1065

NAME/KEY: mat\_peptide

LOCATION: 196..1065

US-08-528-057-45

alignment\_scores:

Quality: 289.00 Length: 173

Ratio: 2.890 Gaps: 6

Percent similarity: 57.803 Percent identity: 39.884

alignment\_block:

US-10-031-904-8 x US-08-528-057-45

Align seg 1/1 to: US-08-528-057-45 from: 1 to: 1304

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144 TGGGTTGCTCTTGGCGGCCATGCTCTCTCTCTCTCTCTCTCTCCGAG 193

34 IncysAnValProGluIuPleuProPheAlaArgProThrAnLeuThr 50

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51 AspAspPheGlu.....PhePr 56

214 .....TTTGAAGCTATGAGCTCTTGTGTAACCAAAACCTACTATGA 257

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73 ro.....PheSerIleIleCysLeuLysAsnSerValTTPThrSer 86

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358 GCTCTGATGACGCGCTGTATATAGAAACATGTCATATATAGGATGC 407

102 oValAnsglyMetAlaHisValIleLys...AspIleGlnPheGlySer 118

408 TTTAAATGGCCAAAGCAGTCCCTGCAAATGGACCTACGACTTGGTTATC 457

118 IuLeuTyTrSerCysProLysGlyTyrArgLeuIleGlySerSerSer 134

458 AGATGACTTATTGTGTAATGAGGTTTACTTAAATTGGTGAAGAAATT 507

135 AlaThrCysAlaIleIleSerGlyAsnThrValIleTyrAspAnLysThrPr 151

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seq\_name: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq:US-08-458-084-3

seq\_documentation\_block:

Sequence 3, Application US/08458084

Patent No. 5624837

GENERAL INFORMATION:

APPLICANT: Fodor, William L

APPLICANT: Rollins, Scott

APPLICANT: Squinto, Stephen P

TITLE OF INVENTION: Chimeric Complement

TITLE OF INVENTION: Inhibitor Proteins

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maurice M. Klee

STREET: 1951 Burr Street

CITY: Fairfield

STATE: Connecticut

COUNTRY: USA

ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 750 Kb storage

COMPUTER: Dell 486/50

OPERATING SYSTEM: DOS 6.2

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,084

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? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Klee, Maurice M.
? REGISTRATION NUMBER: 30,399
? REFERENCE/DOCKET NUMBER: ALX-120
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (203) 254-1400
? TELEFAX: (203) 254-1101
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1530 bases
? TYPE: Nucleic Acid
? STRANDEDNESS: Double
? TOPOLOGY: Linear
? MOLECULE TYPE: cDNA to mRNA
? DESCRIPTION: MCP (CD46) full length cDNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? PUBLICATION INFORMATION:
? AUTHORS: Lublin, D.M.
? AUTHORS: Liszewski, M.K.
? AUTHORS: Post, T.W.
? AUTHORS: Arce, M.A.
? AUTHORS: Lebeau, M.M.
? AUTHORS: Rebentisch, M.B.
? AUTHORS: Lemons, R.S.
? AUTHORS: Seyer, T.
? AUTHORS: Atkinson, J.P.
? TITLE: Molecular cloning and Chromosomal
? TITLE: Localization of Membrane Cofactor
? TITLE: Protein (MCP): Evidence for Inclusion
? TITLE: in the Multi-Gene Family of
? TITLE: Complement-Regulatory Proteins.
? JOURNAL: Journal of Experimental Medicine
? VOLUME: 168
? PAGES: 181-194
? DATE: 1988
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? US-08-458-084-3
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? alignment_scores:
? Quality: 289.00 Length: 173
? Ratio: 2.890 Gaps: 6
? Percent Similarity: 57.803 Percent Identity: 39.884
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? Sequence 3, Application US/08205508
? Patent No. 5627264
?
? GENERAL INFORMATION:
? APPLICANT: Fodor, William L
? APPLICANT: Rollins, Scott
? APPLICANT: Squinto, Stephen P
? TITLE OF INVENTION: Chimeric Complement
? TITLE OF INVENTION: Inhibitor Proteins
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Maurice M. Klee
? STREET: 1951 Burr Street
? CITY: Fairfield
? STATE: Connecticut
? COUNTRY: USA
? ZIP: 06430
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch, 750 Kb storage
? COMPUTER: Dell 486/50
? OPERATING SYSTEM: DOS 6.2
? SOFTWARE: Wordperfect 6.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/205,508
? FILING DATE:
?
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Klee, Maurice M.
? REGISTRATION NUMBER: 30,399
? REFERENCE/DOCKET NUMBER: ALX-120
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (203) 254-1101
? TELEFAX: (203) 254-1400
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1530 bases
? TYPE: Nucleic Acid
? STRANDEDNESS: Double
? TOPOLOGY: Linear
? MOLECULE TYPE: cDNA to mRNA
? DESCRIPTION: MCP (CD46) full length cDNA
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? PUBLICATION INFORMATION:
? AUTHORS: Lublin, D.M.

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AUTHORS: Liszewski, M.K.  
AUTHORS: Post, T.W.  
AUTHORS: Arce, M.A.  
AUTHORS: Lebeau, M.M.  
AUTHORS: Rebentisch, M.B.  
AUTHORS: Lemons, R.S.  
AUTHORS: Seya, T.  
AUTHORS: Atkinson, J.P.  
TITLE: Molecular cloning and Chromosomal  
TITLE: Localization of Membrane Cofactor  
TITLE: Protein (MCP): Evidence for Inclusion  
TITLE: in the Multi-Gene Family of  
TITLE: Complement-Regulatory Proteins.  
JOURNAL: Journal of Experimental Medicine  
VOLUME: 168  
PAGES: 181-194  
DATE: 1988  
US-08-205-508-3

alignment\_scores:  
Quality: 289.00 Length: 173  
Ratio: 2.890 Gaps: 6  
Percent Similarity: 57.803 Percent Identity: 39.884

alignment\_block:  
US-10-031-904-8 x US-08-205-508-3 ..

Align seg 1/1 to: US-08-205-508-3 from: 1 to: 1530

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102 oValAsnGlyMetAlaHisValIleLys...AspLeuInPheGlySerG 118
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358 TTTAAATGGCCCAAGCAGTCCCTGCAATGGGAGCTTACAGTTGGTATC 407
118 InLleLysTySerCysProLysGlyTyArgLeuIleGlySerSerSer 134
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408 AGATGCACTTATTTGTATATGAGGGTATTAATTGATTTGGAGGAATA 457
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458 CTATATTTGGAAGCTTAAAGATCACTACCAATTGGAGCGGTAAAGCCCC 507
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seq\_name: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:US-08-482-148-8

seq\_documentation\_block:

Sequence 8, Application US/08482148  
Patent No. 584/082

GENERAL INFORMATION:  
APPLICANT: Rother, Russell

APPLICANT: Rollins, Scott  
APPLICANT: Squinto, Stephen P

TITLE OF INVENTION: Terminal Complement  
TITLE OF INVENTION: Inhibitor Fusion Genes and Proteins

NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Seth A. Fidel  
STREET: Alexion Pharmaceuticals, 25 Science Park

CITY: New Haven  
STATE: Connecticut

COUNTRY: USA  
ZIP: 06511

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible (Pentium)  
OPERATING SYSTEM: Windows 95 under MS DOS

SOFTWARE: Microsoft Word for Windows  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,148  
FILING DATE: 6/07/95

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: Fidel, Seth A.  
REGISTRATION NUMBER: 38,449

REFERENCE/DOCKET NUMBER: ALX-129.1 Div  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 776 1790  
TELEFAX: (203) 772 3655

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:

LENGTH: 1530 base pairs  
TYPE: Nucleic Acid

STRANDEDNESS: Double  
TOPOLOGY: Linear

MOLECULE TYPE: cDNA to mRNA  
DESCRIPTION: MCP (CD46) full length cDNA

HYPOTHETICAL: No  
ANTI-SENSE: No

ORIGINAL SOURCE:  
ORGANISM: Homo sapiens

PUBLICATION INFORMATION:  
AUTHORS: Lublin, D.M.

AUTHORS: Liszewski, M.K.  
AUTHORS: Post, T.W.

AUTHORS: Arce, M.A.  
AUTHORS: Lebeau, M.M.

AUTHORS: Rebentisch, M.B.  
AUTHORS: Lemons, R.S.

AUTHORS: Seya, T.  
AUTHORS: Atkinson, J.P.

TITLE: Molecular cloning and Chromosomal  
TITLE: Localization of Membrane Cofactor

TITLE: Protein (MCP): Evidence for Inclusion  
TITLE: in the Multi-Gene Family of

TITLE: Complement-Regulatory Proteins.  
JOURNAL: Journal of Experimental Medicine

VOLUME: 168  
PAGES: 181-194

DATE: 1988  
US-08-482-148-8

alignment\_scores:  
Quality: 289.00 Length: 173  
Ratio: 2.890 Gaps: 6

Percent Similarity: 57.803 Percent Identity: 39.884

alignment block:

US-10-031-904-8 x US-08-482-148-8 ..

Align seg 1/1 to: US-08-482-148-8 from: 1 to: 1530

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458 CTATATTGTGAACCTTAAGGATCAGTACATTTGAGAGCGGTAGCCCCC 507
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 15:59:43 ; Search time 1838.24 Seconds  
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Perfect score: 627  
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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3595312

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Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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31	191.4	30.5	227	9	HUMCRIL2	M31231 Human compl
32	178.2	28.4	695	9	HUMCRISF02	L17399 Human compl
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34	177	28.2	227	9	HUMCR102	M31238 Human compl
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ALIGNMENTS

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ACCESSION AX078362  
VERSION AX078362.1 GI:13158031  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 627)  
AUTHORS Au-Young,J., Bandman,O., Tang,Y.T., Yue,H., Azimzai,Y., Burford,N.,  
Baughn,M.R., Lu,D.A., Hillman,J.L., Patterson,C. and Lal,P.  
TITLE Receptors and associated proteins  
JOURNAL Patent: WO 0107612-A 30 01-FEB-2001;  
Incyte Genomics, Inc. (US)  
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BASE COUNT 142 a 173 c 128 g 184 t



Oy	66	aaggaggtctccggcgacgctcaatggcgccttcctcgtctctgaagtgcttcttccttc	125
Db	28	ATGGGCGCCCTCTTCTTCGAAGAAAGCCCGAGCCTGTCCGCCGCCGCGCCGGCTTCCTCC	87
Oy	126	cggcgacttctcgttggtgtcttcctgvcgacctgglttgtct--gclgtcctcttc	182
Db	88	TTCGTGC GGAGAGATCCCTCGTGCGSGTWTGTGCTGCTGTGGCGTGGCGGCGCTGG	147
Oy	183	gatcaatgaagaatgccggaatggttcattttccagcgcttaaacctaactgtatgc	242
Db	148	GGTCAATGCAATGCCCCCAAGATGCTTCCATTTCACAGGCTTACCACCTTAAGTGTAG	207
Oy	243	tttagtttccaatcatggagacatatctgaactatgaatgcgcgcctggtltaclccgaaga	302
Db	208	TTTAGATTTCCTCCATGCGACATATCTGAATGTAAATGCGCCGCTGGTTATTCCGGAAGA	267
Oy	303	ccgctttctatactctgcgttaaataaacctcacgtctcggacaagtgtctaagagaagtgc	362
Db	268	CCGTTTTCTATCATCTGCGCTTAATAAATCTCAATCTGGAAGTGGTCTAAGACAAGTTC	327
Oy	363	cytaaatcatgtcgtatcctccctcagatcccttgaaatgacatgacatgacataagac	422
Db	328	CCTAATATCATAGTGATATCTCTCCATCTCTGAAATGCGATGTGATCAAAAGCG	387
Oy	423	atccagttcggatcccgaattaataattctgtccctaagaagataccgactatggttc	482
Db	388	ATCCAGTTCGGATCCCAAATTAATTTCTGTACTTAAGATACCGACATTTGGTTCC	447
Oy	483	tgcgtgcgcacatgacatcatctcagagaacactgtcataattggagataaataaacctgt	542
Db	448	TGCGTGCACCATGCAATCATCTCATCGATGTAATCTGTCTATTGGGATTAATGAACCTATT	507
Oy	543	ttgtgacag 550	
Db	508		
Db	508	TGTGACAG 515	
RESULT	3		
HSCRTS			
LOCUS	HSCR1S	2376 bp	MRNA linear PRI 22-MAR-1995
DEFINITION	Human CRI mRNA for C3b/C4b receptor secreted form.		
ACCESSION	X14362.Y00812		
VERSION	X14362.1 GI:30197		
KEYWORDS	alternate splicing; C3b/C4b receptor; complement receptor;		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 2376)		
JOURNAL	Hourcade, D.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (29-NOV-1988) Hourcade D., Howard Hughes Medical		
TITLE	Institute, 660 S. Euclid St. Louis Mo, 63110, USA		
FEATURES	2 (bases 1 to 2376)		
LOCUS	Hourcade, D., Wiesner, D.R., Atkinson, J.P. and Holiers, V.M.		
IDENTIFICATION	Identification of an alternative polyadenylation site in the human		
C3b/C4b receptor (complement receptor type 1) transcriptional unit			
and prediction of a secreted form of complement receptor type 1			
J. Exp. Med. 168 (4), 1255-1270 (1988)			
COMMENT	The sequence overlaps with that reported by Klickstein et. al. in		
J. Exp. Med. 165:1095-1112(1987) x05309 and in J. Exp. Med.			
168:1699-1717(1988).			
Location/Qualifiers			
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/clone="CRI-4"			
/haplotypes="CRI-A"			
/cell_line="HL-60"			
<I..1682			

[illegible]

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Qy 322 taaaaactcagctggaagaagtgtaagaagaagtaacatcagtcgtaac 381

Db 187 TAAAAAATCAGTCTGAGCTGCTGCTTAAGAGAGAGTGCAGAGCTAAATCATCTGCTATC 246

Qy 382 ctccagatcctgtaagtgagacatgagatgataaagaacatcagtcgataccaa 441

Db 247 CTCGAGATCCTGTAATGGCATGTGATCAAGACATCAATTCGATCCGATAA 306

Qy 442 ttaaatattctgtcctaagaagataccagactatgttccctcgtccacatgcatca 501

Db 307 TTAATAATCTCTGTACTAAAGATACCGACTATTGGTCTCGTCTGCGACATGATCA 366

Qy 502 tctcaggaacacactgcatctgagataaacaacactggtttgagacg 550

Db 367 TCTCAGGTGATCTGATCTGATTTGGATTAAGAAACACCTATTGTCAGAG 415

LOCUS 6044 bp mRNA linear PRI 30-OCT-1994

DEFINITION chimpanzee complement receptor type one (CRL) mRNA, partial cds.

ACCESSION L24920

VERSION L24920.1 GI:551564

KEYWORDS complement receptor 1.

SOURCE Pan troglodytes cDNA to mRNA.

ORGANISM Pan troglodytes

REFERENCE 1 (bases 1 to 6044)

AUTHORS Birmingham,D., Shen,X.-P., Hourcade,D., Nickells,M.W. and Atkinson,J.P.

TITLE Primary sequence of an alternatively spliced form of CRL. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes

JOURNAL J. Immunol. 153 (2), 691-700 (1994)

FEATURES

source

location/Qualifiers

1..6044

/organism="Pan troglodytes"

/db\_xref="taxon:9598"

1..6044

/gene="CRL"

<1..>6044

/gene="CRL"

/codon\_start=3

/product="complement receptor 1"

/protein\_id="AA51438.1"

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BASE COUNT 1561 a 1496 c 1462 g 1525 t

ORIGIN

Query Match 54.8%; Score 343.4; DB 9; Length 6044;

Best Local Similarity 90.0%; Pred. No. 6.2e-90;

Matches 368; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 142 tgccttgagcgccctggtgtgtctgctctcctccatcagatcagtcgccg 201

Db 7 TCTGCGCGGTTGTGGTCTGCTGCGCTGCGGCTGGGCTGATGCAATGCCAG 66

Qy 202 aatgctccattgcccagcctacacactaactgagtcagttccattccattgga 261

Db 67 AATGGCTTCATTTGCCAGGCTACCAACCTAAGATGATGATTTGAGTTCCATGGGA 126

Qy 262 catatcgaactatgaatgcgcctgttattccggaaagccgltttatcatctgcc 321

Db 127 CATATCTGAACATGATGATGCGCCCTGGTTATTATGGAAGACCGTTTCTATCATCTGCC 186

Qy 322 taaaaactcagctggaagaagtgtaagaagaagtaacatcagtcgtaac 381

Db 187 TAAAAAATCAGTCTGAGCTGCTGCTTAAGAGAGAGTGCAGAGCTAAATCATCTGCTATC 246

Qy 382 ctccagatcctgtaagtgagacatgagatgataaagaacatcagtcgataccaa 441

Db 247 CTCGAGATCCTGTAATGGCATGTGATCAAGACATCAATTCGATCCGATAA 306

Qy 442 ttaaatattctgtcctaagaagataccagactatgttccctcgtccacatgcatca 501

Db 307 TTAATAATCTCTGTACTAAAGATACCGACTATTGGTCTCGTCTGCGACATGATCA 366

Qy 502 tctcaggaacacactgcatctgagataaacaacactggtttgagacg 550

Db 367 TCTCAGGTGATCTGATCTGATTTGGATTAAGAAACACCTATTGTCAGAG 415

RESULT 7

BABCORE 1688 bp mRNA linear PRI 07-MAY-1996

LOCUS Baboon cynocephalus complement receptor mRNA, partial cds.

DEFINITION

ACCESSION L77977

VERSION L77977.1 GI:1301608

KEYWORDS complement C3b, complement receptor; glycoposphatidylinositol-linked protein.

SOURCE Papio cynocephalus

ORGANISM Papio cynocephalus

REFERENCE 1 (bases 1 to 1688)

AUTHORS Birmingham,D., Logar,C.M., Shen,X.-P. and Chen,W.

TITLE The baboon erythrocyte complement receptor is a glycoposphatidylinositol-linked protein encoded by a homologue of the human CRL-like genetic element

JOURNAL Unpublished (1996)

FEATURES

source

location/Qualifiers

1..1688

/organism="Papio cynocephalus"

/db\_xref="taxon:9556"

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EPPTISNDGFYSNNRASHNCTVNTYQCHGDBGDLIELYGBESITYCTSDPDVYQ

WSSPPRCLISNKTAPAEVENA.IRVGNKSFSLIEIVFRQPGVWVGSTTVOCOT

NGRMGKPLRCSVQCPPEILLGHEHTPSHONFSPGOEVEFSCPEGYDLRGAASLHC

TPGQWSPAPRCVSCDFFOLKPHGVLPPLNLGAKYFVCDIEFRLKGSAS

HCYLAACMLMNSVPCVOCIRCPNPLINRHTGTPGDIPLYKEISYACDTPHDS

GMPFNLTGESINCTSDPOGNGWSSPAPRCCLSVPAACPHHPKIONGHDIGHSVLY

LPQMTISYICDPGLLVGKGFICTDQGISMDRHCYKNSVSPFLPMNGISKELEMK

KVYHGDVYVTLKCEDGYTLLEGSPWQQQADRDMDPLACTGSRHADALIVGSSSTIF

FILIIIFLSWIIILHKRGNNHKKPEVEVALIHLSOGSSVHPPTIQTENSRVLP"





MgCl2: 1.5 mM  
KCl: 50 mM  
Tris-HCl: 10 mM  
pH: 9.3

FEATURES  
Derived from dbEST (genbank accession T66823).

source  
1.389  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="890.2 CR from top of Chr1 linkage group"  
STS  
primer\_bind 25..149  
primer\_bind 25..149  
BASE COUNT 114 a 67 c 92 g 112 t 4 others  
ORIGIN

Query Match 48.9%; Score 306.4; DB 11; Length 389;  
Best Local Similarity 95.8%; Pred. No. 2.8e-79;  
Matches 345; Conservative 0; Mismatches 10; Indels 5; Gaps 3;  
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369 ctgaactatgaatgc---cgccctgttattcgcgaagaccgttt-ctatcatctg-cc 310  
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322 taataaactcagtcgtgcaagtcgtaaggaacagtcgaacgtaaatcgtcgtatc 381  
|||||  
309 TAAAAAAGCTCACTGCGACAGTGTAAAGACAGTCAAGCTCAATCATGTCGTGTAAC 250  
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382 ctccagatccctgtgtaatgcatgacatgtgataaagacatccagttcgcgaacaa 441  
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249 CTCGAGANCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 190  
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442 ttaaatattctgtctcgaagatcaccgactcattgttctcgtctgcgacatgacaa 501  
|||||  
189 TTAATATNTCTTGCTCTAAAGATACCGACATGCTGCTCTGCTGCTGCTGCTGCTGCT 130  
|||||  
502 tctcaggaacacatgcatcttggtggaataaacaacctgttttgacagtgagttgaat 561  
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129 TCTCAGGCAACACTGCTCATTTGGATATATAAACCTGTTGTGACAGTGAATGAAT 70  
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562 atgcattcctattcttcttaccgatacatcttaatttctcgcgataataaactctt 621  
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69 ATGCATTCCTATTCTTTTACCGATACATCTCTATTCTTCTGGAATATATAAATCTT 10  
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RESULT 11  
G27827/c 389 bp DNA linear STS 29-JUN-1996

INITIATION human STS SHGC-33387, sequence tagged site.  
ACCESSION G27827  
VERSION G27827.1 GI:1396546  
KEYWORDS STS: STS sequence; primer; sequence tagged site.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Contact: Richard M. Myers  
JOURNAL Stanford Human Genome Center (SHGC)  
Unpublished Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myerseshgc.stanford.edu

Primer A: CCAGAGAAAATTAGATGTATCGG  
Primer B: CTGCTCTGCCACATGATC  
STS size: 125

## PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:  
Template: 25 ng  
Primer: each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer:  
MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T66823  
-- Washington University/Merck EST sequence.

FEATURES  
source  
1.389  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="1"  
STS  
primer\_bind 25..149  
primer\_bind 25..149  
BASE COUNT 114 a 67 c 92 g 112 t 4 others  
ORIGIN

Query Match 48.9%; Score 306.4; DB 11; Length 389;  
Best Local Similarity 95.8%; Pred. No. 2.8e-79;  
Matches 345; Conservative 0; Mismatches 10; Indels 5; Gaps 3;  
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322 taataaactcagtcgtgcaagtcgtaaggaacagtcgaacgtaaatcgtcgtatc 381  
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309 TAAAAAAGCTCACTGCGACAGTGTAAAGACAGTCAAGCTCAATCATGTCGTGTAAC 250  
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502 tctcaggaacacatgcatcttggtggaataaacaacctgttttgacagtgagttgaat 561  
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129 TCTCAGGCAACACTGCTCATTTGGATATATAAACCTGTTGTGACAGTGAATGAAT 70  
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562 atgcattcctattcttcttaccgatacatcttaatttctcgcgataataaactctt 621  
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69 ATGCATTCCTATTCTTTTACCGATACATCTCTATTCTTCTGGAATATATAAATCTT 10  
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RESULT 12  
CHPCR1Y 1731 bp mRNA linear PRI 12-OCT-1994  
LOCUS CHPCR1Y  
DEFINITION Pan troglodytes mRNA sequence, 3' end of ORF.  
ACCESSION U24922  
VERSION U24922.1 GI:557728  
KEYWORDS Pan troglodytes CDNA to mRNA.  
SOURCE Pan troglodytes  
ORGANISM Pan troglodytes



REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Pan. 1 (phases 1 to 1731)
AUTHORS	Birmingham, D.J., Shen, X.P., Hourcade, D., Nickells, M.W. and Atkinson, J.P.
TITLE	Primary sequence of an alternatively spliced form of CRI. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes
JOURNAL	J. Immunol. 153 (2), 691-700 (1994)
MEDLINE	94292799
FEATURES	Location/Qualifiers 1 1731

CDS <1. .1571

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DDVOYINGSPAGDIIIPNCKTPYVNGHSLVSDNRSEFSLNVEYFQCPGVYMGKPG
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GPRLGKGSASGACVLAAGKALMNSVYCCEDIFCPNPAALINHHGHTPLGDIYKKE
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1572. ->/1/31

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BASE COUNT	469 a	395 c	403 g	463 t
ORIGIN				1 others

Query Match	48.4%;	Score 303.2;	DB 9;	Length 1731;
Best Local Similarity	97.5%;	Pred. No. 3.3e-78;		
Matches 308; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0.

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Db 1 CTGATGAGTTTGAGTTCCTCCATTGGACATATCGAACTPATAGAATCCGCCCTGTATT 60

QY 295 ccggaagacgcgttctatcatcgtgccataaaactcaagtctygacaagtgtctaagaca 354  
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
61 ATGGAAGACCACTTTCTATCATCTGCCCTAAAAAOTCAGTGTGGACAAGTCGTGAGGACA 120

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Oy      355 agtgcacaagtaatcatgtctgaatccctcagatccctggaatgcatggacattgaa 414
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Db      121 AGTGCACAAGTAATCATGTCTGATCCGCCAGATCCTGTGAATGGCATGGTCATGTGA 180
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Qy 415 tcaagacatccagtcgcgatcccaatlaatatcttgcctaagataccgactca 474  
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Db 181 TCAAGACATCCAGTTCGGATCCCAATLAATATCTTGTACTAAGATACCAGACTCA 240

Oy 475 ttgtcttcgcgtcgccacatgcatcattcaggaacactgtlcatattygataataaa 53  
|||||  
Db 241 TTGCTTCCTCGTCCACATGCATCATTCAGGCAACACTGTCAATTGGGAATAATAAA 300

Oy	535 cacctgtttgtgacag	550
Db	301 CACCTGTTTGTGCAG	316

## RESULT 13

LOCUS	A86593	591 bp	DNA	linear	PAT 21-JAN-2000
DEFINITION	Sequence 2 from Patent WO9839433.				
ACCESSION	A86593				
VERSION	A86593.1	GI:6735168			
KEYWORDS	.				

SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	1 (bases 1 to 591)
AUTHORS	Smith R.A. and Cox V.F.
TITLE	COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL	Patent: WO 9839433-A 2 11-SEP-1998.
FEATURES	SMITH RICHARD ANTONY GOWDIN (GB); ADPROTECH PLC (GB)
source	Location/Qualifiers 1..591 /organism="unidentified" /db_xref="taxon:32644"
BASE COUNT	132 a 159 c 148 g 152 t
ORIGIN	

Query Match	42.6%;	Score 267.4;	DB 6;	Length 591;
Best Local Similarity	-83.3%;	Pred. No. 9.4e-68;		
Matches 304; Conservative	0;	Mismatches 61;	Indels 0;	Gaps 0;

186 caatgcaatgtcccggaatggtcttccattgtccagggcctaccacctaactgtagcttc 245

Db 4 CAGTCCAAACGCTCCGGAAATGCGTGCCGCTTCCGCGGCCCGACCAACCTGACATGATGAATTT 63

QY 246 gagttcccatgtggacatatctgaactatgaatgcgcccgtgtattccggaagacg 305

Db 64 GAGTCCCGATCGGTACTACTGACIACGAATGCCGCCGGGTATTAGCGGCCGCCGCC 123

QY 306 ttcttatcatctgcctaaanaactcagtcctgacaaagtctaaagacaagtgcacaacgt 365

Db 124 TTTTTCATCATCTGCCGAAAACCTCTGCTGACCTGGTGTAAAGACCGTTGCCGACGT 183  
Qy 366 aaatcatgtcgtaatccctccagaatcctgtgaatgcatgcatgacatgtgatcaagaacatc 425

Db 184 AATCTTGTCTGAATCCGCCAGATCCGGTTACGCGCATGTGCATGTGATCAAAAGGCAATC 213

QY 426 cagtcgcgatcccaatataatctctgtcctaagaataccgactcaatggttcctcg 485

Db 244 CAGTTCCGTTCCCAATTAAATATTCTTCTACTAAAGTTACCGTCTGATTTGTTCCCTCC 30

QY 486 tctgcacatgatcatctcagcgacacactgcatcttggtataataaacactgtttgt 54

Db 304 AGGCTACATGCATCACTCTGGTACTACTGTCATTGGGATATATGAACACCGATTGT 36  
QY 546 gacag 550

Db 364 GACCG 368

LOCUS	A86601	591 bp	DNA	
DEFINITION	Sequence 10 from Patent WO9839433.			
			linear	PAT 21-JAN-2000

REFERENCE	1 (bases 1 to 591)
AUTHORS	Smith, R.A. and Cox, V.F.
TITLE	COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE SEQUENCES
JOURNAL	Patent: WO 9839433-A 10 11-SEP-1998;
FEATURES	SMITH RICHARD ANTHONY GOMDIN (GB); ADPROTECH PLC (GB); Location/Qualifiers

Source	1. .591
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/db_xref="taxon:32644"	
BASE COUNT	127 a 159 c 151 g 154 t
ORIGIN	

Query Match 42.68; Score 267.4; DB 6; Length 591;



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 16:37:29 ; Search time 176.28 Seconds  
(without alignments)  
6106.792 Million cell updates/sec

Title: US-10-031-904-30

Perfect score: 627  
Sequence: 1 cggactcagaaggacttcc.....ataataaaacttaaccga 627

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
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17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	627	100.0	627	22	AAFS8602
2	352	56.1	6951	10	AAAG91477
3	352	56.1	6951	12	AAQ11642
4	352	56.1	6951	20	AAZ38150
5	352	56.1	7313	22	AAI58380
6	351.8	56.1	7821	23	AA564474
7	348	55.5	6951	14	AAQ41867
8	341	54.4	7028	22	ABA09026
9	341	54.4	7028	22	AAI60166

10	273.2	43.6	9038	23	AA564290
11	269.4	43.0	2796	23	AA564473
12	267.4	42.6	591	19	AAV53262
13	267.4	42.6	591	19	AAV53269
14	267.4	42.6	591	19	AAV53270
15	267.4	42.6	591	19	AAV53271
16	267.4	42.6	591	19	AAV53272
17	267.4	42.6	591	19	AAV53273
18	247.8	39.5	2798	23	AA564289
19	218.6	34.9	5420	12	AAQ11643
20	218.6	34.9	5420	20	AA38151
21	156.4	24.9	1477	18	AA790306
22	156.4	24.9	3302	22	AAH34933
23	156.4	24.9	3308	21	AA718275
24	153.6	24.5	396	21	AAQ4275
25	124.6	19.9	125	19	AA11827
26	120	19.1	1437	23	AA564286
27	120	19.1	1437	23	AA564470
28	117.6	18.8	1530	16	AAQ99106
29	117.6	18.8	1530	16	AA703339
30	117.6	18.8	1546	12	AAQ10864
31	116.6	18.6	1878	17	AA746065
32	103.4	16.5	1244	12	AAQ14919
33	103.4	16.5	1659	12	AAQ14915
34	103.4	16.5	1991	12	AAQ14916
35	103.4	16.5	9888	24	ABL33241
36	88.8	14.2	1848	22	AAQ03255
37	88.8	14.2	1848	22	AAQ08170
38	88	14.0	7821	23	AA564474
39	87.4	13.9	945	17	AA717599
40	87.4	13.9	1134	17	AA717598
41	87.4	13.9	1134	17	AA717595
42	87.4	13.9	1134	17	AA717596
43	87.4	13.9	1134	17	AA717597
44	84.8	13.5	9888	24	ABL33240
45	79.4	12.7	1104	15	AAQ58894

#### ALIGNMENTS

RESULT 1	
ID	AAFS8602
standard:	cdna: 627 bp.
AAFS8602:	
24-APR-2001 (first entry)	
Human RECAP polynucleotide, SEQ ID NO: 30.	
Human; RECAP; receptors and associated proteins; cerebroprotective; neurotrophic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV; antidiabetic; immunostimulant; immunomodulator; antinflammatory; antihypoid; immunosuppressive; nephrotoxic; antipruritic; thymoleptic; cytostatic; antibacterial; virucide; fungicide; protozoacide; antarteriosclerotic; hepatotropic; gene therapy; infection; cancer; ss.	
antiserotrophic; gene therapy; infection; cancer; ss.	
Homo sapiens.	
WO200107612-A2.	
01-FEB-2001.	
21-JUL-2000; 2000MO-US20035.	
21-JUL-1999; 99US-0145332.	
07-OCT-1999; 99US-0158578.	
12-NOV-1999; 99US-0165192.	
(INCYTE -) INCYTE GENOMICS INC.	
Au-Young J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;	



key	Location/Qualifiers
FT sig_peptide	28..147
FT	/tag= a
FT	/note= "putative"
FT mat_peptide	148..6144
FT	/*tag= b
FT	/product= C3b/Cab receptor
XX	
PN	W09105047-A.
XX	
PD	18-APR-1991.
XX	
PE	25-SEP-1990;
XX	
PR	26-SEP-1989;
XX	
PR	26-SEP-1990;
XX	
XX	(TCCEL-) T CELL SCI INC.
PA	(UYJO ) JOHNS HOPKINS UNIVERSITY.
PA	(BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
XX	
XX	Fearon DT, Klickstein LB, Wong MW, Carson GR, Hoh M, Concino MF, Makrides SC, Marsh HC;
XX	

T 22-FEB-2000 (first entry)

DT 22-FEB-2000 (first entry)

DE Human C3b/C4b receptor (CRI) protein encoding DNA.  
 XX C3b/C4b receptor; CRI protein; cell-surface protein; erythrocyte; human;  
 KM complement regulatory activity; complement pathway enzyme; tissue damage;  
 KM reperfusion injury; Arthus reaction; myocardial infarct; inflammation;  
 KM heart condition; autoimmune disorder; diagnostic; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US981481-A.  
 XX  
 PD 09-NOV-1999.  
 XX  
 PF 06-JUN-1995; 95US-0470652.  
 XX  
 PR 03-APR-1989; 89US-0332865.  
 PR 06-DEC-1974; 74US-0350238.  
 PR 24-FEB-1993; 93US-0026134.  
 PR 01-APR-1988; 88US-0176532.  
 XX  
 (UYTO ) UNIV JOHNS HOPKINS.  
 (BGHM ) BRIGHAM & WOMEN'S HOSPITAL.  
 (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.  
 PA  
 PI Conclno MF, Wong MW, Makrides SC, Klickstein LB, Fearon DT, Ip SH;  
 PI Marsh HC, Carson GR;  
 XX  
 DR WPI; 1999-63357/54.  
 DR P-PSDB; AAI55751.  
 XX  
 PT A human C3b/C4b receptor (CRI) protein having antiinflammatory and  
 PT cardiant activity -  
 XX  
 PS Disclosure: Fig 1A-P; 87pp; English.  
 XX  
 CC The invention relates to a human C3b/C4b receptor (CRI) protein. The CRI  
 CC protein or fragment is expressed as a cell-surface protein on the surface  
 CC of a non-human cell and exhibits a complement regulatory activity of full  
 CC -length human CRI as expressed on erythrocytes. The CRI function in vivo  
 CC may be mediated through the inhibition of complement pathway enzymes. The  
 CC soluble CRI protein exhibits a complement regulatory activity, and this  
 CC may be used to prevent reperfusion injury, inhibit Arthus reaction, and  
 CC neutrophil mediated tissue damage, and reduce myocardial infarct size,  
 CC and inflammation. The CRI protein and its fragments can also be used in  
 CC the treatment of conditions which involve unwanted complement activity,  
 CC e.g. shock lung, tissue damage due to burn, or ischemic heart conditions,  
 CC and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-  
 CC -CRI antibodies are used in assays, and diagnostics. The present sequence  
 CC represents a DNA encoding the human CRI protein.  
 CC  
 CC Sequence 6951 BP; 1802 A; 1680 C; 1661 G; 1808 T; 0 other;  
 CC  
 CC Query Match 56.1%; Score 352; DB 20; Length 6951;  
 CC Best Local Similarity 84.0%; Pred. No. 1.3e-96;  
 CC Matches 410; Conservative 0; Mismatches 75; Indels 3; Gaps 1;  
 CC  
 QY 66 acggaggtcccgccgagctatgagcctccgctcgtctcgcgaggtcccttctctcc 125  
 DB 28 atgggggctctctcccaagaagccgagcctcgtcggccgagccgagctctcc 87  
 QY 126 cggcgcttccctggtctctcgtcggcgccctgtgtgtc--gctgctctctctcc 182  
 DB 88 ttctgtcggagagatccctgtcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 147  
 QY 183 gatcaatgaatgctccggaatgctcattgcccagagcctaccacaaactatgatgac 242  
 DB 148 ggtcaatgaatgctccggaatgctcattgcccagagcctaccacaaactatgatgac 207  
 QY 243 ttggaattcccatgagacatatcgaactatgaatgacgagcctgtgttttcggaaga 302  
 DB 208 ttggaattcccatgagacatatcgaactatgaatgacgagcctgtgttttcggaaga 267

QY 303 ccgtttctatcatctgctcctaaataaactcagctcgtgacaagtgtcaaggacagtgcaaa 362  
 DB 268 ccgtttctatcatctgctcctaaataaactcagctcgtgacagtggtgtcaaggacagtgcaaa 327  
 QY 363 cgttaatcagctgtatcctcctcagatcctgtgagatgacagcagcctgtatataagac 422  
 DB 328 cgttaatcagctgtatcctcctcagatcctgtgagatgacagcagcctgtatataagac 387  
 QY 423 atccagctcgtatcccaataataatctctgtcctaaagataccagctcattgtgtcc 482  
 DB 388 atccagctcgtatcccaataataatctctgtcctaaagataccagctcattgtgtcc 447  
 QY 483 tctgtcgtcagatcagctatcctcagacacatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 542  
 DB 448 tctgtcgtcagatcagctatcctcagacacatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 507  
 QY 543 tgtgacag 550  
 DB 508 tgtgacag 515  
 XX  
 RESULT 5  
 AAI58380  
 ID AAI58380 standard; cDNA; 7313 BP.  
 XX  
 AC AAI58380;  
 XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 XX Human polynucleotide SEQ ID NO 583.  
 XX  
 DE Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW Leukaemia; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 XX 26-DEC-2000; 2000MO-US34263.  
 XX  
 PF 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AD, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Driamanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR P-PSDB; AAM39224.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Claim 1; SEQ ID NO 583; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide



[illegible]









AAV53262  
 ID AAV53262 standard; DNA: 591 BP.  
 XX  
 AC AAV53262;  
 XX  
 DT 18-JAN-1999 (first entry)  
 XX  
 DE Complement receptor type 1-like sequence CM7 DNA.  
 XX  
 KW Complement receptor type-1; CRI; CM7; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO983943-A1.  
 XX  
 PF 11-SEP-1998.  
 XX  
 PF 05-MAR-1998; 98WO-GB00727.  
 XX  
 PR 05-MAR-1997; 97GB-0004519.  
 XX  
 PA (ADPR-) ADPROTECH PLC.  
 XX  
 PI Cox VF, Mossakowska DEL, Smith RAG;  
 XX  
 DR WPI: 1998-506358/43.  
 DR P-PSDB; AAW79236.  
 XX  
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PT used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 XX  
 PS Claim 22; Page 42-43; 67pp; English.  
 XX  
 CC This DNA sequence encodes CM7 (see AAW79236), a protein that consists  
 CC of the short consensus repeats (SCR) 1 and 2 from the complement  
 CC receptor type 1 (CRI) fused to the SCR3 of CRI-like pseudogene (see  
 CC AAW79247). CM7 DNA was constructed using plasmid pBI1013-5, which  
 CC codes for SCR1-3 of CRI, by site-directed mutagenesis using 3 pairs  
 CC of oligonucleotides (see AAV53263-65) that introduced 10 amino acid  
 CC changes to the native SCR3 sequence corresponding to changes  
 CC observed in the CRI-like pseudogene (Crlpse). pProcSCR1-3CM7  
 CC carrying the CM7 DNA construct was used to transform *Escherichia*  
 CC coli BL21(DE3), and CM7 was purified from solubilised inclusion  
 CC bodies. The invention provides DNA sequences (see AAV53262 and  
 CC AAV53269-79) encoding novel soluble engineered CRI polypeptides (see  
 CC AAV53236-47) such as CM7 that act as complement inhibitors with  
 CC functional complement inhibitory, including anti-haemolytic,  
 CC activity. These can be used to treat a disease or disorder  
 CC associated with inflammation or inappropriate complement activation,  
 CC such as neurological disorders (e.g. multiple sclerosis and  
 CC Parkinson's disease), disorders of inappropriate or undesirable  
 CC complement activation (e.g. xenograft rejection), inflammatory  
 CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC post-ischaemic reperfusion conditions, infection or sepsis,  
 CC immune complex disorders and autoimmune diseases (e.g. Rheumatoid  
 CC arthritis, proliferative nephritis and myasthenia gravis), and  
 CC reproductive disorders.  
 CC  
 SO Sequence 591 BP; 132 A; 159 C; 148 G; 152 T; 0 other;

Query Match 42.6%; Score 267.4; DB 19; Length 591;  
 Best Local Similarity 83.3%; Pred. No. 2.5e-71;  
 Matches 304; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
 QY 186 caatgcaatgtccggaatgcttcattgcagcctcaaccaactatgatgactt 245

DB 4 cagttgcaacgctccggaatgctgcgctcgcccgcaaccaactgactgatgatt 63  
 QY 246 gagttccatgtggacaatctgaactatgaatgcgcgcctgttattccggaagccg 305  
 DB 64 gagttccggaatcggtactctcctgaactaagaatgcgcgcgggtatagcgccgcg 123  
 QY 306 ttcttcatcctgcgtcaaaaactcagtcctggacaagtgttaaggacaagtgcacgt 365  
 DB 124 ttcttcatcctgcgtcaaaaactcctgtcgtgactcgtgttaaggacgcttgcgagct 183  
 QY 366 aactcatgtctgatatcctccagatcctctggaatgagatgacatgtgttcaagaacatc 425  
 DB 184 aactctgtctgatatcctccagatcctgtaaacgcatgtgtgcatgtgatacaagcattc 243  
 QY 426 cagttcgatcccaaatlaattctcttgcctaagaagatcagactatgttcttcgcg 485  
 DB 244 cagttcggttcccaaatlaattctcttgcctaagaagatcagactatgttcttcctcc 303  
 QY 486 tctgcacaatgataatcctcgaagaacactgtcatttggataataaaccactgttgt 545  
 DB 304 agcgtacacatgataatcctcgtgtgatactgtcatttggataatgaacaccgattgt 363  
 QY 546 gacag 550  
 DB 364 gaccg 368

RESULT 13  
 AAV53269  
 ID AAV53269 standard; DNA: 591 BP.  
 XX  
 AC AAV53269;  
 XX  
 DT 18-JAN-1999 (first entry)  
 XX  
 DE Complement receptor type 1-like sequence CM1 DNA.  
 XX  
 KW Complement receptor type-1; CRI; CM1; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy; ss.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO983943-A1.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PF 05-MAR-1998; 98WO-GB00727.  
 XX  
 PR 05-MAR-1997; 97GB-0004519.  
 XX  
 PA (ADPR-) ADPROTECH PLC.  
 XX  
 PI Cox VF, Mossakowska DEL, Smith RAG;  
 XX  
 DR WPI: 1998-506358/43.  
 DR P-PSDB; AAW79237.  
 XX  
 PT Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PT used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation  
 XX  
 PS Claim 22; Page 44; 67pp; English.  
 XX  
 CC This DNA sequence encodes CM1 (see AAW79237), a protein that consists  
 CC of the short consensus repeats (SCR) 1 and 2 from complement  
 CC receptor type 1 (CRI) fused to an SCR3 (see AAW79242) in which 5 amino  
 CC acids were altered to those found in the SCR3 of the CRI-like

CC pseudogene (Cripse) putative product. CM1 DNA was constructed by  
 CC site-directed mutagenesis (see AAV53263) of plasmid pDB1013-5, which  
 CC codes for SCRI-3 of CRI. pProSCRI-3CM1 carrying CM1 DNA was used  
 CC to transform *Escherichia coli* BL21(DE3), and CM1 was purified from  
 CC solubilised inclusion bodies. The invention provides DNA sequences  
 CC (see AAV53262 and AAV53269-79) encoding novel soluble engineered CRI  
 CC polypeptides (see AAV53236-47) such as CM1 that act as complement  
 CC inhibitors with functional complement inhibitory, including  
 CC anti-haemolytic, activity. These can be used to treat a disease or  
 CC disorder associated with inflammation or inappropriate complement  
 CC activation, such as neurological disorders (e.g. multiple sclerosis  
 CC and Parkinson's disease), disorders of inappropriate or undesirable  
 CC complement activation (e.g. xenograft rejection), inflammatory  
 CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC post-ischaemic reperfusion conditions, infection or sepsis,  
 CC immune complex disorders and autoimmune diseases (e.g. Rheumatoid  
 CC arthritis, proliferative nephritis and myasthenia gravis), and  
 CC reproductive disorders.

XX Sequence 591 BP; 127 A; 159 C; 151 G; 154 T; 0 other;

Query Match 42.6%; Score 267.4; DB 19; Length 591;  
 Best Local Similarity 83.3%; Pred. No. 2.5e-71;  
 Matches 304; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 186 caatgcaatgtccggagatggtcttcattgacggcctaccacctaactgacttt 245  
 DB 4 cagtgcaacgctccggaatggtcgtcgccgcgcgcgcacacccgactgactgaattt 63  
 QY 246 gagttcccatgtggacatactgaactaataatgacgcgcctgtgtatccggaagacg 305  
 DB 64 gagtcccgatcgtgactactactgaactgaatgacgcgcgcgggttaagagcgccgcg 123  
 QY 306 tttctatcatctgcctctctctctgaactgaactgaactgaactgaactgaactgaact 365  
 DB 124 tttctatcatctgcctctctctctgaactgaactgaactgaactgaactgaactgaact 183  
 QY 366 aaatcatgtcttaactcccgacactctgtgaatgacatgacatgacatgacatgacatgac 425  
 DB 184 aaatctgtctgaatccgc 243  
 QY 426 cagttcgatcccaataataatctgtctctctctctctctctctctctctctctctctct 485  
 DB 244 cagttcgatcccaataataatctgtctctctctctctctctctctctctctctctctct 303  
 QY 486 tctgccaatgcatcatct 545  
 DB 304 agcgctacatgcatcatct 363  
 QY 546 gacag 550  
 DB 364 gacgc 368

RESULT 14  
 AAV53270  
 ID AAV53270 standard; DNA: 591 BP.

AAV53270;

18-JAN-1999 (first entry)

Complement receptor type 1-like sequence CM2 DNA.

XX Complement receptor type-1; CRI; CM2; complement; inhibitor;  
 KW anti-haemolytic; multiple sclerosis; Parkinson's disease;  
 KW xenograft rejection; inflammation; Crohn's disease; asthma;  
 KW pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
 KW autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
 KW myasthenia gravis; reproductive disorder; therapy; ss.  
 XX Homo sapiens.

OS Synthetic.

XX WO9839433-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-GH00727.

XX 05-MAR-1997; 97GB-0004519.

XX (ADPR-) ADPROTECH PLC.

XX Cox VF, Mossakowska DEI, Smith RMG;

XX WPI, 1998-506358/43.

XX P-PSDB; AAW79238.

XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
 PT used to treat disorders and diseases associated with inflammation or  
 PT inappropriate complement activation

XX Claim 22; Page 45; 67pp; English.

XX This DNA sequence encodes CM2 (see AAW79238), a protein that consists  
 CC of the short consensus repeats (SCR) 1 and 2 from complement  
 CC receptor type 1 (CRI) fused to an SCR3 (see AAW79243) in which 4 amino  
 CC acids were altered to those found in the SCR3 of the CRI-like  
 CC pseudogene (Cripse) putative product. CM2 DNA was constructed by  
 CC site-directed mutagenesis (see AAV53264) of plasmid pDB1013-5, which  
 CC codes for SCRI-3 of CRI. pProSCRI-3CM2 carrying CM2 DNA was used  
 CC to transform *Escherichia coli* BL21(DE3), and CM2 was purified from  
 CC solubilised inclusion bodies. The invention provides DNA sequences  
 CC (see AAV53262 and AAV53269-79) encoding novel soluble engineered CRI  
 CC polypeptides (see AAV53236-47) such as CM2 that act as complement  
 CC inhibitors with functional complement inhibitory, including  
 CC anti-haemolytic, activity. These can be used to treat a disease or  
 CC disorder associated with inflammation or inappropriate complement  
 CC activation, such as neurological disorders (e.g. multiple sclerosis  
 CC and Parkinson's disease), disorders of inappropriate or undesirable  
 CC complement activation (e.g. xenograft rejection), inflammatory  
 CC disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
 CC post-ischaemic reperfusion conditions, infection or sepsis,  
 CC immune complex disorders and autoimmune diseases (e.g. Rheumatoid  
 CC arthritis, proliferative nephritis and myasthenia gravis), and  
 CC reproductive disorders.

XX Sequence 591 BP; 134 A; 158 C; 146 G; 153 T; 0 other;

Query Match 42.6%; Score 267.4; DB 19; Length 591;  
 Best Local Similarity 83.3%; Pred. No. 2.5e-71;  
 Matches 304; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 186 caatgcaatgtccggagatggtcttcattgacggcctaccacctaactgacttt 245  
 DB 4 cagtgcaacgctccggaatggtcgtcgccgcgcgcgcacacccgactgactgaattt 63  
 QY 246 gagttcccatgtggacatactgaactaataatgacgcgcctgtgtatccggaagacg 305  
 DB 64 gagtcccgatcgtgactactactgaactgaatgacgcgcgcgggttaagagcgccgcg 123  
 QY 306 tttctatcatctgcctctctctctgaactgaactgaactgaactgaactgaactgaact 365  
 DB 124 tttctatcatctgcctctctctctgaactgaactgaactgaactgaactgaactgaact 183  
 QY 366 aaatcatgtcttaactcccgacactctgtgaatgacatgacatgacatgacatgacatgac 425  
 DB 184 aaatctgtctgaatccgc 243  
 QY 426 cagttcgatcccaataataatctgtctctctctctctctctctctctctctctctctct 485  
 DB 244 cagttcgatcccaataataatctgtctctctctctctctctctctctctctctctctct 303

QY 486 tctgcacatgcatactcaggaacactgtcattgggataataaacactgtt 545  
DB 304 agcgctacatgcatactcgtgtgtaactgttggaataaagaaacagactt 363  
OY 546 gacag 550  
DB 364 gaccg 368

RESULT 15  
AAV53271

ID AAV53271 standard; DNA: 591 BP.

AC AAV53271;

DT 18-JAN-1999 (first entry)

DE Complement receptor type 1-like sequence CM3 DNA.

CM Complement receptor type-1; CR1; CM3; complement; inhibitor;  
anti-haemolytic; multiple sclerosis; Parkinson's disease;  
xenograft rejection; inflammation; Crohn's disease; asthma;  
pancreatitis; post-ischaemic reperfusion; infection; sepsis;  
KM autoimmune disease; rheumatoid arthritis; proliferative nephritis;  
KM myasthenia gravis; reproductive disorder; therapy; ss.

OS Homo sapiens.  
XX Synthetic.

PN W09839433-A1.

XX 11-SEP-1998.

PD 05-MAR-1998; 98WO-GB00727.

XX 05-MAR-1997; 97GB-0004519.

PR (ADPR-) ADPROTECH PLC.

PA Cox VF, Mossakowska DEI, Smith RAG;

XX WPI: 1998-506358/43.

DR P-PDB; AAV79239.

XX Soluble polypeptide comprising short consensus repeats from LHR-A -  
used to treat disorders and diseases associated with inflammation or  
inappropriate complement activation

XX Claim 22: page 46; 67pp; English.

CC This DNA sequence encodes CM2 (see AAW79239), a protein that consists  
of the short consensus repeats (SCR) 1 and 2 from complement  
receptor type 1 (CR1) fused to an SCR3 (see AAW79244) in which 1 amino  
acid was altered to that found in the SCR3 of the CR1-like  
pseudogene (Cripse) putative product. CM3 DNA was constructed by  
site-directed mutagenesis (see AAV53265) of plasmid pB1013-5, which  
codes for SCR1-3 of CR1. pBiosCR1-3CM3 carrying CM3 DNA was used  
to transform Escherichia coli BL21(DE3), and CM3 was purified from  
solubilised inclusion bodies. The invention provides DNA sequences  
(see AAV53262 and AAV53269-79) encoding novel soluble engineered CR1  
polypeptides (see AAV53236-47) such as CM3 that act as complement  
inhibitors with functional complement inhibitory, including  
anti-haemolytic, activity. These can be used to treat a disease or  
disorder associated with inflammation or inappropriate complement  
activation, such as neurological disorders (e.g. multiple sclerosis  
and Parkinson's disease), disorders of inappropriate or undesirable  
complement activation (e.g. xenograft rejection), inflammatory  
disorders (e.g. Crohn's disease, asthma, and acute pancreatitis),  
post-ischaemic reperfusion conditions, infection or sepsis,  
immune complex disorders and autoimmune diseases (e.g. rheumatoid  
arthritis, proliferative nephritis and myasthenia gravis), and  
reproductive disorders.

SQ Sequence 591 BP; 131 A; 160 C; 149 G; 151 T; 0 other:

Query Match 42.6%; Score 267.4; DB 19; Length 591;  
Best Local Similarity 83.3%; Pred. No. 2.5e-71;  
Matches 304; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

OY 186 caatgcaatgtccggaaatgagcttcacattgccaagcctaccacctaactgatgactt 245  
DB 4 cagtgcaacgctccggaaatgagcttcacattgccaagcctaccacctaactgatgactt 63  
OY 246 gagttcccatgtggacatctgaactatgaatgcgcgcctgtttatccgaaagccg 305  
DB 64 gagtcccgatcggtaacctgaactaagaaatgcgcgcctgtttatccgaaagccg 123  
OY 306 ttctcatcatcgtgcctaaactcaagctcgtggaacagtgtaaggaacagtgcaacgt 365  
DB 124 ttctcatcatcgtgcctaaactcaagctcgtggaacagtgtaaggaacagtgcaacgt 183  
OY 366 aaatcatgtcgttaatcctccagatcctgtgtaatgcatgacatgtgataaagacatc 425  
DB 184 aaatctgtcgttaatcctccagatcctgtgtaatgcatgacatgtgataaagacatc 243  
OY 426 cagttcggaatcccaatataattctgtcctaaagataccgacctggttctctcg 485  
DB 244 cagttcggtcccaatataattctgtcctaaagataccgacctggttctctcg 303  
OY 486 tctgcacatgcatactcaggaacactgtcattgggataataaacactgtt 545  
DB 304 agcgctacatgcatactcgtgtgtaactgttggaataaagaaacagactt 363  
OY 546 gacag 550  
DB 364 gaccg 368

Search completed: October 9, 2002, 17:40:21  
Job time: 3772 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 16:04:33 ; Search time 1594.28 Seconds  
(without alignments)  
5308.096 Million cell updates/sec

Title: US-10-031-904-30

Perfect score: 627

Sequence: 1 cgagactcagaagagacttc.....ataataaaatttaaccga 627

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estbta:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	71.0	465	10	BE552138
2	443.6	70.7	832	10	BE240184
3	435	69.4	443	9	AT240881
4	393.6	62.8	444	9	AT1718588
5	352	56.1	1063	10	BM477528
6	344.8	55.0	356	9	AT1735459
7	326.8	52.1	440	10	H73873
8	307	49.0	345	10	T66824
9	306.4	48.9	389	10	T66823
10	270.4	43.1	541	10	T83269
11	268.6	42.8	433	9	AT1735085
12	212.8	33.9	577	10	BE077250
13	212.8	33.9	614	9	AA107525
14	212.8	33.9	658	10	BT697900
15	212.8	33.9	795	10	BT455761
16	212.8	33.9	807	10	BT078162
17	211.2	33.7	601	9	AA212152

18	208	33.2	773	10	BT556660
19	206.8	33.0	722	10	BT696340
20	205	32.7	488	10	BE023537
21	205	32.7	569	10	BT693880
22	205	32.7	684	9	BB613937
23	204.8	32.7	643	9	AW912091
24	203.4	32.4	525	9	AA286570
25	203.4	32.4	650	9	AW610808
26	201.8	32.2	1646	11	AK004825
27	199.6	31.8	735	10	T27695
28	195	31.1	739	10	BE243080
29	194.6	31.0	861	10	BF178335
30	194	30.9	388	10	BG146321
31	194	30.9	403	9	AW610947
32	194	30.9	409	9	AW012541
33	192.8	30.7	441	9	AW825298
34	189.2	30.2	303	10	RO1561
35	184.6	29.4	469	9	AA261275
36	184.6	29.4	981	10	BE917021
37	184.2	29.4	889	10	BF166939
38	182.6	29.1	387	9	AW211552
39	180	28.7	519	10	BF159845
40	170.2	27.1	431	10	BF015454
41	166	26.5	770	10	BF124847
42	164.4	26.2	3859	11	AK017702
43	159.4	25.4	419	9	AA756782
44	157	25.0	397	9	AA314773
45	156.4	24.9	300	9	AU100130

#### ALIGNMENTS

RESULT 1  
BE552138/c  
LOCUS  
DEFINITION  
BE552138  
LOCUS  
hm29g02.x1 NCI\_CGAP\_Kid11 Homo sapiens cDNA clone IMAGE:3184323 3'  
similar to gb:Y00816.cdsl COMPLEMENT RECEPTOR TYPE 1 PRECURSOR  
(HUMAN); mRNA sequence.

ACCESSION  
BE552138  
VERSION  
BE552138.1  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens

REFERENCE  
1 (bases 1 to 465)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL, send email to:  
info@image.lnl.gov  
Seq primer: -40UP from Glibco  
High quality sequence stop: 456.

FEATURES  
source  
Location/Qualifiers  
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/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not 1; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Kid3 was





DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
g94e04.x1 NCI_CGAP_Kid3 Homo sapiens CDNA clone IMAGE:1867134 3'	AI240861.1	GI:3836278	(HUMAN); mRNA sequence.	Homo sapiens	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	NCI-CGAP	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA library preparation: M. Bento Soares, Ph.D.									
CDNA library Arrayed by: Greg Lennon, Ph.D.									
DNA Sequencing by: Washington University Genome Sequencing Center									
Clone distribution: NCI-CGAP clone distribution information can be									
found through the I.M.A.G.E. Consortium/HLN at:									
<a href="http://www.bio.lnml.gov/db/brp/image/image.html">www.bio.lnml.gov/db/brp/image/image.html</a>									
Insert length: 625									
Seq primer: -40up from Gidco									
High quality sequence stop: 373.									
Location/Qualifiers									
1.443									
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/db_xref="taxon:9606"									
/clone="IMAGE:1867134"									
/clone_lib="NCI_CGAP_Kid3"									
/lab_host="DH10B"									
/note="Organ: Kidney; Vector: pRT7D-Pac (Pharmacia) with									
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st									
strand cDNA was primed with a Not I - oligo(dT) primer,									
double-stranded cDNA was ligated to Eco RI adaptors									
(Pharmacia), digested with Not I and cloned into the Not									
I and Eco RI sites of the modified pRT73 vector. mRNA									
source: 2 pooled kidneys. Library went through one round									
of normalization. Library constructed by Bento Soares and									
M. Fatima Bonaldo.									
BASE COUNT	131 a	80 c	104 g	128 t					
ORIGIN									
Query Match	69.4%;	Score 435;	DB 9;	Length 443;					
Best Local Similarity	98.9%;	Pred. No. 5.6e-110;							
Matches 438; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;					
Oy 185 tcaatcgaaatgcgcgaatgctccatcttgcgcagagctcaactaactatgatctt 244									
Db 443 TCATGCAATGTCGGGAATGGGCTTCCATTGTCGACGGCTACCACTTAATGATGATC 384									
Oy 245 tgaattccatttggacatctctgaactatgaatgcgcgccttggtatctccggaagcc 304									
Db 383 TGAATTTCATTGGGACATATCTGAACATGAAGCCGCCCTGTGTTATTCGGAAGACC 324									
Oy 305 gtcttcatactatgtcctaaataactcagctctgcgaagctgtaaggaagaatgcgaagc 364									
Db 323 GTTTTCATATATCTGGCTTAAATAACTCAAGTCTGACCAAGTCTTAAGGACAAAGTCAAGC 264									
Oy 365 taatcatctgcgaatctctccagatctcttgaatggaatggaatgtaacatgtaacaaat 424									
Db 263 TAAATCATGTCGTAAATCTTCAGATCTCTGTGAATGGCATGTGCACATGTGATCAAAAGACAT 204									
Oy 425 ccaattcgatcccaaatcaatatctctgtccctaaagaataacagatctatgttccctc 484									
Db 203 CCAATTGCGATGCCAATTAATTAATTTCTTGTCCTAAAGATAGCGACTCATGTGGTTCCTC 144									
Oy 485 gtctgcacaatgcatcatctcgaagcaaacctgtcatcttggagataataaacaacctgttg 544									

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	143	CTCTGCCACATGCATCATCTCAGGACACATGTCATTTGGGATTAATAAACACCTGTTGG	444 bp	MRNA	linear	EST 10-JUN-1999						
QY	545	tgacagatgagatggaatatgcatctccattcttccattccacgatacatctcaatttctct	444 bp	MRNA	linear	EST 10-JUN-1999						
Db	83	TGACAGGAGGTGAAATATGATGCTTCATTTCTTTTACGATACATTTCAATTTTCTCT	444 bp	MRNA	linear	EST 10-JUN-1999						
QY	605	ggaataataaaatcttaaccga 627	444 bp	MRNA	linear	EST 10-JUN-1999						
Db	23	GGATATATATAAAATCTTTACCA 1	444 bp	MRNA	linear	EST 10-JUN-1999						
RESULT	4	AI1718588	444 bp	MRNA	linear	EST 10-JUN-1999						
LOCUS		AI1718588/c	444 bp	MRNA	linear	EST 10-JUN-1999						
DEFINITION		as46h01.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone	444 bp	MRNA	linear	EST 10-JUN-1999						
ACCESSION		IMAGE:2320273 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE	444 bp	MRNA	linear	EST 10-JUN-1999						
VERSION		1 PRECURSOR (HUMAN);, mRNA sequence.	444 bp	MRNA	linear	EST 10-JUN-1999						
KEYWORDS		AI1718588	444 bp	MRNA	linear	EST 10-JUN-1999						
SOURCE		AI1718588.1 GI:5035844	444 bp	MRNA	linear	EST 10-JUN-1999						
ORGANISM		human.	444 bp	MRNA	linear	EST 10-JUN-1999						
REFERENCE		Homo sapiens	444 bp	MRNA	linear	EST 10-JUN-1999						
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	444 bp	MRNA	linear	EST 10-JUN-1999						
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	444 bp	MRNA	linear	EST 10-JUN-1999						
		1 (bases 1 to 444)	444 bp	MRNA	linear	EST 10-JUN-1999						
		Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,	444 bp	MRNA	linear	EST 10-JUN-1999						
		Kritman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin	444 bp	MRNA	linear	EST 10-JUN-1999						
		,J., Moore,B., Schellenberg,K., Stepec,M., Tan,F., Theising,B.,	444 bp	MRNA	linear	EST 10-JUN-1999						
		White,Y., Wyllie,T., Waterston,R. and Wilson.R.	444 bp	MRNA	linear	EST 10-JUN-1999						
		Washington University School of Medicine	444 bp	MRNA	linear	EST 10-JUN-1999						
		4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	444 bp	MRNA	linear	EST 10-JUN-1999						
		Tel: 314 286 1800	444 bp	MRNA	linear	EST 10-JUN-1999						
		Fax: 314 286 1810	444 bp	MRNA	linear	EST 10-JUN-1999						
		Email: estewatson.wustl.edu	444 bp	MRNA	linear	EST 10-JUN-1999						
		This clone is available royalty-free through LNL ; contact the	444 bp	MRNA	linear	EST 10-JUN-1999						
		IMAGE Consortium (info@image.lnl.gov) for further information.	444 bp	MRNA	linear	EST 10-JUN-1999						
		Seq primer: -400p from Glenco.	444 bp	MRNA	linear	EST 10-JUN-1999						
FEATURES		Location/Qualifiers	444 bp	MRNA	linear	EST 10-JUN-1999						
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		/db_xref="taxon:9606"	444 bp	MRNA	linear	EST 10-JUN-1999						
		/clone IMAGE:2320273"	444 bp	MRNA	linear	EST 10-JUN-1999						
		/clone_lib="Barstead aorta HPLRB6"	444 bp	MRNA	linear	EST 10-JUN-1999						
		/sex="male"	444 bp	MRNA	linear	EST 10-JUN-1999						
		/dev_stage="adult, age 64"	444 bp	MRNA	linear	EST 10-JUN-1999						
		/lab_host="DH10b (phage resistant)"	444 bp	MRNA	linear	EST 10-JUN-1999						
		/note="Organ: aorta; Vector: pTR73D-Pac (Pharmacia) with a	444 bp	MRNA	linear	EST 10-JUN-1999						
		modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st	444 bp	MRNA	linear	EST 10-JUN-1999						
		strand cDNA was primed with a Not I - oligo(dT) primer [5'	444 bp	MRNA	linear	EST 10-JUN-1999						

Query Match	56.1%;	Score 352;	DB 10;	Length 1063;
Best Local Similarity	84.0%;	Pred. No. 8.3e-87;		

REFERENCE 1 (bases 1 to 1063)  
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strusberg, Ph.D.

Plate: LLAM12272 row: n column: 04  
High quality sequence stop: 749.

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1..10635
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5554371"
/clone_id="N1H.MGC.85"
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/lab_host="DH108 (phage-resistant)"
/notes="Organ: lymph. Vector: pCMV-Sport6. Site: 1: NotI.
Site: 2: SalI. Cloned unidirectionally. oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies

```

[illegible]

Query Match	56.1%;	Score 352;	DB 10;	Length 1063;
Best Local Similarity	84.0%;	Pred. No. 8.3e-87;		

RESULT	6
LOCUS	A1735459/c
DEFINITION	A1735459 356 bp mRNA linear EST 14-JUN-1999 at11h03.x1 Barstead aorta HPRb6 Homo sapiens cDNA clone IMAGE:3354837 3' similar to gb:Y00816_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN);, mRNA sequence.

REFERENCE	1 (bases 1 to 356)
AUTHORS	Hillier, L., Allen, M., Bon

**TITLE** Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,  
White,T., Wylie,T., Waterston,R. and Wilson,R.  
**JOURNAL** Washu-NCI human EST Project  
**COMMENT** Unpublished (1997)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL ; contact the

Seq primer: -400P from G	Location/Qualif
FEATURES	

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/db_xref="taxon
/clone="IMAGE:2

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	Query Match	49.0%;	Score 307;	DB 10;	Length 346;
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	Matches 340;	Conservative 0;	Mismatches 3;	Indels 3;	Gaps 3;
QY	72	tctccgcgcgcgcctatgagcgccctccgtctgtgagcgtgtcccttctcccgagcgc	131		
Db	1	TCGCCGGCCCGCTCATGCG-CNTCCGCGTCGTCGAGCGTCCCTTCCTCCCGCGCC	59		
QY	132	ttcttcgggtgtgctctctgagcgccctggtgtgtgtcgtgcctccttcgcgatcaatgc	191		
Db	60	TTTCTCGGGTTGCTTCGCGGGCCCTGGTGTGTGCTGTGCTTCCTTCCTCCATCAATGC	119		
QY	192	aatgtcccggaatggtcctcaatttgcagagcctaccacaactaactatgaattgaatt	251		
Db	120	AATGTCCCGGATGGCTTCATTTGCCAGGCGTACCAACACTAATCATATGATTT	179		
QY	252	cccatitggacaatatctgaacatgaatgcgcgcct-ggllattccggaagacgltttc	310		
Db	180	CCCATTTGGGACATATCTGCAACTATGAATGCCGCGCTGGGTTATTCCGGAAGACGTTTTC	239		
QY	311	tatactcgcctaaaaaacctcagtcctgagaaagtgtctaagagacaagtgcacaagt-aaat	369		
Db	240	TATCATCTGCTTAAAAAACAATCAGCTTGAGACAAAGTCTAAGGACAAGTGCAACGTAAAT	299		
QY	370	catctgcgaatcctccagatcctgtgaatgagcattgccaatgtgat	415		

Query Match	48.9%	Score 306.4	DB 10	Length 389
Best Local Similarity	95.8%	Pred. No. 2,6e-74		
Matches 345	Conservative 0	Mismatches 10	Indels 5	Gaps 3
QY	267	ctgaactatgatgc---cgcccggtatctcggaaacccgtttt-ctatcatctg-cc	321	
DBb	369	ctgaactatgatgcgcccccctggttaantccggagaccggtttctatcatctgcgcc	310	
QY	322	taaaaactcagctctgtgacaagctgctaaggacaagtcgaaagtaaatcatgtcgaatc	381	
DBb	309	taaaaactcagctctgtgacaaagtccttaaggacaagtcgaatcgaatcgaatcgaatc	250	
QY	382	ctccagatccctgtgaatgagcatggtgacaatgtgatcaagaagatccagttcggatcccaa	441	
DBb	249	ctccagatccctgtgaatgagcatggtgacaatgtgatcaagaagatccagttcggatcccaa	190	

Oy	442	ttaaataatcttcgtcctaagataccgactcaattggltccctgcgtcgcacaatgatca	501
Db	189	TTAAATANTCTTCTTAAGAAGATACCGACATCATGGTGTCGTGATGCACATGATCA	130
Oy	502	tctaaagcaacactgycatttgygataataaacacctglttlygcaagyagtftgaat	561
Db	129	TCTAGCGACAACCTGTCATTGGGATAATAAACACCCTGTTGGAAGAGCAATGTAAT	70
Oy	562	atgattccattttcttaaccgatacatcttaatttttctcygaataataaaactt	621
Db	69	ATGATTCCTAATTTCTTTACCGATACATCTCAATTTTTCTCTGATAATAAAAATCTT	10

RESULT	10	
LOCUS	783269	
DEFINITION	783269 541 bp mRNA linear EST 16-MAR-1995	
ACCESSION	U44111.1	Soares fetal liver spleen cDNA clone
VERSION	IMAGE:110780.5	similar to gb:Y00815_cds1 COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (HUMAN);, mRNA sequence.
KEYWORDS	783269	
SOURCE	783269.1	GI:711557
	EST.	
	human.	

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
1 (bases 1 to 541)					
Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkins, M., Holman					
M., Hultman, M., Kuecha, T., Le-M., Lennon, G., Marra, M., Parsons, J.,					
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston					
, R., Williamson, A., Woldmann, P. and Wilson, R.					
The WashU-Merck EST Project					
Unpublished (1995)					
Contact: Wilson RK					

Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: gese@watson.wustl.edu  
Insert Size: 791  
High quality sequence stops: 300 Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pTV73D (Pharmacia with a modified polylinker; Site1: Pac I; Site2: Eco RI 1st strand cDNA was primed with a Pac I - oligo(dT) prime 15', AACTCGACAGATTAATTAAGACGCTCTTTTCTTTTCTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac and Eco RI sites of the modified pTV73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fátima Bonafide."

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				Gaps 5

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ACCESSION	A1735085
VERSION	A1735085.1 GI:5056545
KEYWORDS	Est.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE  
AUTHORS  
Hillier, L., Allen, M., Bowles, L., Dubnue, T., Gelsel, G., Jost, S.,  
Kizman, D., Kucaba, T., Lacy, M., Le, N., Lemmon, G., Martin, M.,  
J., Moore, B., Schnellberg, K., Stepoe, M., Tan, F., Theising, B.,  
White, Y., Wylie, T., Waterston, R. and Wilson, R.  
TITLE  
JOURNAL  
WashU-NCI human EST Project  
unpublished (1997)  
COMMENT  
Contact: Wilson RK

Washington University School of Medicine  
4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: -40UP from Gibco  
High quality sequence stop: 60.  
Location/Qualifiers

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/note="Organ: aorta; Vector: pT730-Pac (Pharmacia) With
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TGTTACGAATCTGAAGTGGAGGCGGCCCTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adapters
[5' AATTGGATCGAAC 3' and 5' GTTGGATCG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT7T3 vector. Library constructed by Bob
Barstead."

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KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 614)
AUTHORS	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheinberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The Mashu-HMMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:343245 Seq primer: -28M13 rev1 from Amersham High quality sequence stop: 431.
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396	aatgcatcagcagcatgtagatacaaaacatccagcttcgtagatccccaattaaatctctgt 455
336	aatggcttggatgacatgtatcacacacagcatttcagtttggaatcccgatttaattatcttct 395
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[illegible]

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Qy 516 gtacattggtgataataaacacccgttttga 547

Db 483 GTTGATTGGGATCTACTGAGGCACCATTTGTGTA 514

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<b>DEFINITION</b>	603171169pf1 NCI_GGAP_Mam5 Mus musculus CDNA clone IMAGE:5251289 5' , mRNA sequence.

REFERENCE  
TITLE  
AUTHORS  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus  
1 (bases 1 to 79)  
NTH-MGC <http://mgc.ncl.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

FEATURES	Location/Qualifiers
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Search completed: October 9, 2002, 17:37:05  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2002, 15:16:43 ; Search time 32.99 Seconds  
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Title: US-10-031-904-30

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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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3	267.4	42.6	605	2	US-08-769-967A-33	Sequence 33, Appl
4	218.6	34.9	5420	6	5256642-3	Patent No. 5256642
5	218.6	34.9	5420	6	5472939-3	Patent No. 5472939
6	156.4	24.9	1304	2	US-08-528-057-45	Sequence 45, Appl
7	148	23.6	1247	2	US-08-528-057-41	Sequence 41, Appl
8	118.4	18.9	1545	4	US-08-139-195-1	Sequence 1, Appl
9	117.6	18.8	1530	1	US-08-458-084-3	Sequence 3, Appl
10	117.6	18.8	1530	1	US-08-205-008-3	Sequence 3, Appl
11	117.6	18.8	1530	1	US-08-482-148-8	Sequence 8, Appl
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13	117.6	18.8	1530	5	PCT-US95-02945-3	Sequence 3, Appl
14	117.6	18.8	1546	6	5514787-1	Patent No. 5514787
15	116.6	18.6	1878	2	US-08-435-149-17	Sequence 17, Appl
16	104.2	16.6	1986	2	US-08-528-057-43	Sequence 43, Appl
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21	88.8	14.2	903	1	US-08-310-416A-11	Sequence 11, Appl
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23	88.8	14.2	1848	4	US-09-475-460A-31	Sequence 31, Appl
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 Patent No. 5256642  
 APPLICANT: FEARON, DOUGLAS T.; KLICKSNEIN, LLOYD B.; WONG,  
 WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
 H.; MAKIDES, SAVVAS; MARSH, HENRY C., JR.  
 TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
 RECEPTOR 1 (C1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF  
 USE THEREOF  
 NUMBER OF SEQUENCES: 30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/588,128  
 FILING DATE: 24-SEP-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 412,745  
 FILING DATE: 26-SEP-1989  
 APPLICATION NUMBER: 332,865  
 FILING DATE: 03-APR-1989  
 APPLICATION NUMBER: 176,532  
 FILING DATE: 01-APR-1988  
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APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG, NITIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
; MARRIDES, SAVVAS; MARSH, HENRY C., JR.  
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT  
; MEDICATED DISORDERS  
; NUMBER OF SEQUENCES: 30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/138,825  
; FILING DATE: 19-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 588,128  
; FILING DATE: 24-SEP-1990  
; APPLICATION NUMBER: 412,745  
; FILING DATE: 26-SEP-1989  
; APPLICATION NUMBER: 332,865  
; FILING DATE: 03-APR-1989  
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; FILING DATE: 01-APR-1988  
; SEQ ID NO:1:  
; LENGTH: 6951  
5472939-1

Query Match 56.1%; Score 352; DB 6; Length 6951;  
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QY 483 tcgtcccaatgataatctcaggaacagctgatttggaataaacaacctgtt 542  
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RESULT 3  
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; Patent No. 5859223  
; GENERAL INFORMATION:  
; APPLICANT: Mossakowska, Danuta E.I.  
; APPLICANT: Smith, Richard A.G.  
; APPLICANT: Dodd, Ian  
; APPLICANT: Freeman, Anne Mary  
; TITLE OF INVENTION: Soluble CRI Derivatives  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporate Intellectual Property  
; STREET: P.O. Box 1539  
; CITY: King of Prussia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/769,967A  
; FILING DATE:  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/440,569  
; FILING DATE: 15-May-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: King, William T.  
; REGISTRATION NUMBER: 30,954  
; REFERENCE/DOCKET NUMBER: P30423C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 270-5090  
; TELEFAX: (610) 270-5090  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 605 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; US-08-769-967A-33

Query Match 42.6%; Score 267.4; DB 2; Length 605;  
Best Local Similarity 83.3%; Pred. No. 1.4e-76;  
Matches 304; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 186 caatgcaatgctccggaatgcttccattgccaaggctcaacaactaactgtactt 245  
Db 7 CAGTGCACGCTCCGGAATGCTGCGTTCGCGCGCCGCCGACCAACTGATGTAATT 66  
QY 246 gagtttcccatggaacatactgaaactgaaatgcgcctggttattccggaagcgg 305  
Db 67 GAGTTCCTCCGATCGGTACTCTGAACTGCAATGCGCGCGGTTATGCGCGCCCG 126  
QY 306 ttctctacatcgtccctaaactaactcagtcggaacagtgtaaggaacagtgcaagct 365  
Db 127 TTTTCTATCATCTTGCTCGAATAAATCTCTGTGTGAGCTGTGCTAAGGACCGTTGCGAGCT 186

366 aatcatctcgaatccctccagatccctgtgaatgcatgcatatgataaagacatc 425  
187 AATCTTGTCGTAATCCGCCAGATCCGCTTAACGGCATGTCGATGATATAAGGCATC 246  
426 cagctcgaatcccaataataatctctgtcctaaaggataccgaatcattgctcctcg 485  
247 CAGTTCGGTCCCAATTAATATCTTGTACTAAGGTTACCGCTGATGGTTCCTCC 306  
486 tctgcacatgcatcatctcgaagcaacatgcatcttgggataataaacacgttctgt 545  
307 AGCGTACTGATCATCTCTGGTGATCTGATCTGATTTGGATTAAGAACACCGATTGT 366  
QY 546 gacag 550  
DB 367 GACCG 371

RESULT 4  
5256642-3  
PATENT NO. 5256642  
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.  
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT  
RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF  
USE THEREOF  
NUMBER OF SEQUENCES: 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/588,128  
FILING DATE: 24-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 412,745  
FILING DATE: 26-SEP-1989  
APPLICATION NUMBER: 332,865  
FILING DATE: 03-APR-1989  
APPLICATION NUMBER: 176,532  
FILING DATE: 01-APR-1988  
SEQ ID NO: 3  
LENGTH: 5420

Query Match 34.9%; Score 218.6; DB 6; Length 5420;  
Best Local Similarity 74.5%; Pred. No. 2.6e-60;  
Matches 275; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 181 cgaatcgaatgcaatgctccggaatgcttccattgacgagccctaccacctaactgaty 240  
2674 ctgctacatgtaaacaccagagcaggttccattgacgagccctaccacctaactgaty 2733  
QY 241 acttgagttcccatggaacatctgaactatgaatgacgagccctggttttccgga 300  
DB 2734 acttgagttcccatggaacatctgaactatgaatgacgagccctggttttccgga 2793  
QY 301 gacggtttctatcatctcctaaataatctctgtcctaaaggataaccgactatggt 360  
DB 2794 aaatggttctatctcctcgtcctaaataatctctgtcctaaaggataaccgactatggt 2853  
QY 361 aacgtaaatcatgctgaatccctccagatcctgtgaatgcatgcatatgataaag 420  
DB 2854 gacgaataatcatgctgaatccctccagatcctgtgaatgcatgcatatgataaag 2913  
QY 421 acatcgaatcgaatcccaataataatctctgtcctaaaggataaccgactatggt 480  
DB 2914 ataacaggttgcgaacaggttaataatctctgtcctaaaggataaccgactatggt 2973  
QY 481 cctgctgcgaatcgaatcctcgaagcaacatgcatcttgggataataaacacgtg 540  
DB 2974 cccatctactactgtctcgtcgaagcaatgcatcagtgataaagaagcaccta 3033  
QY 541 ttgtgaca 549  
DB 3034 ttgtgaga 3042

RESULT 5  
5472939-3  
PATENT NO. 5472939  
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,  
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN  
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.  
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT  
MEDiated DISORDERS  
NUMBER OF SEQUENCES: 30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/138,825  
FILING DATE: 19-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 588,128  
FILING DATE: 24-SEP-1990  
APPLICATION NUMBER: 412,745  
FILING DATE: 26-SEP-1989  
APPLICATION NUMBER: 332,865  
FILING DATE: 03-APR-1989  
APPLICATION NUMBER: 176,532  
FILING DATE: 01-APR-1988  
SEQ ID NO: 3  
LENGTH: 5420

Query Match 34.9%; Score 218.6; DB 6; Length 5420;  
Best Local Similarity 74.5%; Pred. No. 2.6e-60;  
Matches 275; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 181 cgaatcgaatgcaatgctccggaatgcttccattgacgagccctaccacctaactgaty 240  
DB 2674 ctgctacatgtaaacaccagagcaggttccattgacgagccctaccacctaactgaty 2733  
QY 241 acttgagttcccatggaacatctgaactatgaatgacgagccctggttttccgga 300  
DB 2734 acttgagttcccatggaacatctgaactatgaatgacgagccctggttttccgga 2793  
QY 301 gacggtttctatcatctcctaaataatctctgtcctaaaggataaccgactatggt 360  
DB 2794 aaatggttctatctcctcgtcctaaataatctctgtcctaaaggataaccgactatggt 2853  
QY 361 aacgtaaatcatgctgaatccctccagatcctgtgaatgcatgcatatgataaag 420  
DB 2854 gacgaataatcatgctgaatccctccagatcctgtgaatgcatgcatatgataaag 2913  
QY 421 acatcgaatcgaatcccaataataatctctgtcctaaaggataaccgactatggt 480  
DB 2914 ataacaggttgcgaacaggttaataatctctgtcctaaaggataaccgactatggt 2973  
QY 481 cctgctgcgaatcgaatcctcgaagcaacatgcatcttgggataataaacacgtg 540  
DB 2974 cccatctactactgtctcgtcgaagcaatgcatcagtgataaagaagcaccta 3033  
QY 541 ttgtgaca 549  
DB 3034 ttgtgaga 3042

RESULT 6  
US-08-528-057-45  
Sequence 45, Application US/08528057  
Patent No. 5846715  
GENERAL INFORMATION:  
APPLICANT: PURCELL, Damian F. J.  
APPLICANT: RUSSELL, Sarah M.  
APPLICANT: MCKENZIE, Ian F. C.  
TITLE OF INVENTION: CD46 VARIANTS  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESS: Foley & Lardner



RESULT 8  
US-08-139-195-1  
; Sequence 1, Application US/08139195  
; Patent No. 6218520  
; GENERAL INFORMATION:  
; APPLICANT: Atkinson, John P.  
; TITLE OF INVENTION: RECOMBINANTLY PRODUCED HUMAN MEMBRANE  
; TITLE OF INVENTION: COPOLYMER PROTEIN (MCP)  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 1100 Peachtree Street, Suite 2800  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-4530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/139,195  
; FILING DATE: 20-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/948,350  
; FILING DATE: 21-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/384,210  
; FILING DATE: 21-JUL-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: W0100CON  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)-815-6508  
; TELEFAX: (404)-815-6555  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1545 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Human t-Cell Line HSB2  
US-08-139-195-1

Query Match 18.9%; Score 118.4; DB 4; Length 1545;  
Best Local Similarity 83.8%; Pred. No. 2.5e-28;  
Matches 134; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 44 tctgtcactcctcggaataacaggggtctccggcgctcattagggcctccgcgcg 103  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||  
DB 1 tctgtcctcctcgcggaataacaggggtctccggcgctcattagggcctccgcgcg 60  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||  
QY 104 tctgtcactcctcggaataacaggggtctccggcgctcattagggcctccgcgcg 163  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||  
DB 61 cccggagtgctcctcctcgcggaataacaggggtctccggcgctcattagggcctccgcgcg 120  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||  
QY 164 gctgtcctcctcctcgcggaataacaggggtctccggcgctcattagggcctccgcgcg 203  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||  
DB 121 gctgtcctcctcctcgcggaataacaggggtctccggcgctcattagggcctccgcgcg 160  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||

RESULT 9  
US-08-458-084-3  
; Sequence 3, Application US/08458084  
; Patent No. 5624837

GENERAL INFORMATION:  
; APPLICANT: Fodor, William L.  
; APPLICANT: Rollins, Scott  
; APPLICANT: Squinto, Stephen P.  
; TITLE OF INVENTION: Chimeric Complement  
; TITLE OF INVENTION: Inhibitor Proteins  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maurice M. Klee  
; STREET: 1951 Burr Street  
; CITY: Fairfield  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06430  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 750 Kb storage  
; COMPUTER: Dell 486/50  
; OPERATING SYSTEM: DOS 6.2  
; SOFTWARE: WordPerfect 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,084  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Klee, Maurice M.  
; REGISTRATION NUMBER: 30,399  
; REFERENCE/DOCKET NUMBER: ALX-120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (203) 254-1101  
; TELEFAX: (203) 254-1101  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1530 bases  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; MOLECULE TYPE: cDNA to mRNA  
; DESCRIPTION: MCP (CD46) full length cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; AUTHORS: Lublin, D.M.  
; AUTHORS: Liszewski, M.K.  
; AUTHORS: Post, T.W.  
; AUTHORS: Arce, M.A.  
; AUTHORS: Lebeau, M.M.  
; AUTHORS: Rebentisch, M.B.  
; AUTHORS: Lemons, R.S.  
; AUTHORS: Seya, T.  
; TITLE: Molecular cloning and Chromosomal  
; TITLE: Localization of Membrane Cofactor  
; TITLE: Protein (MCP): Evidence for Inclusion  
; TITLE: in the Multi-Gene Family of  
; TITLE: Complement-Regulatory Proteins  
; JOURNAL: Journal of Experimental Medicine  
; VOLUME: 168  
; PAGES: 181-194  
; DATE: 1988  
US-08-458-084-3

Query Match 18.8%; Score 117.6; DB 1; Length 1530;  
Best Local Similarity 84.6%; Pred. No. 4.5e-28;  
Matches 132; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 44 tctgtcactcctcggaataacaggggtctccggcgctcattagggcctccgcgcg 103  
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DB 1 tctgtcctcctcgcggaataacaggggtctccggcgctcattagggcctccgcgcg 60  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||  
QY 104 tctgtcactcctcctcgcggaataacaggggtctccggcgctcattagggcctccgcgcg 163  
||||| ||||||| ||||| ||||| ||||||| ||||||| ||||| ||||| ||||| |||||

Db 61 CCGCGAGTGTCCCTTCCTTCGCGCCCTTCCTCGGGTTCCTTCGCGCGCCAGTGT 120

Qy 164 gctgcgtctcctctctctccgataabcaatgtccc 199

Db 121 GCTGCGTACTCTTCCTCCAGTGCCTGTGAGAGCC 156

RESULT 10  
 US-08-205-508-3  
 Sequence 3, Application US/08205508  
 Patent No. 5627264  
 GENERAL INFORMATION:  
 APPLICANT: Scott, William L.  
 APPLICANT: Rollins, Scott  
 APPLICANT: Suinto, Stephen P.  
 TITLE OF INVENTION: Chimeric Complement  
 Inhibitor Proteins  
 TITLE OF INVENTION: Inhibitor Proteins  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Maurice M. Klee  
 STREET: 1951 Burr Street  
 City: Fairfield  
 STATE: Connecticut  
 COUNTRY: USA  
 ZIP: 06430  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 750 Kb storage  
 COMPUTER: Dell 486/50  
 OPERATING SYSTEM: DOS 6.2  
 SOFTWARE: WordPerfect 6.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/205,508  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Klee, Maurice M.  
 REGISTRATION NUMBER: 30,399  
 REFERENCE/DOCKET NUMBER: ALX-120  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (203) 255-1400  
 TELEFAX: (203) 254-1101  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1530 bases  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Linear  
 MOLECULE TYPE: cDNA to mRNA  
 DESCRIPTION: MCP (CD46) Full Length cDNA  
 HYPOTHEITICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 PUBLICATION INFORMATION:  
 AUTHORS: Lublin, D.M.  
 AUTHORS: Liszewski, M.K.  
 AUTHORS: Post, T.W.  
 AUTHORS: Arce, M.A.  
 AUTHORS: Lebeau, M.M.  
 AUTHORS: Rebentisch, M.B.  
 AUTHORS: Lemons, R.S.  
 AUTHORS: Seva, T.  
 AUTHORS: Atkinson, J.P.  
 TITLE: Molecular cloning and Chromosomal  
 TITLE: Localization of Membrane Cofactor  
 TITLE: Protein (MCP): Evidence for Inclusion  
 TITLE: in the Multi-Gene Family of  
 TITLE: Complement-Regulatory Proteins.  
 JOURNAL: Journal of Experimental Medicine  
 VOLUME: 168  
 PAGES: 181-194  
 DATE: 1988

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US-08-205-508-3

Query Match      18.8% ; Score 117.6 ; DB 1 ; Length 1530.
Best Local Similarity 84.6% ; Pred. No. 4,56-28 ;
Matches 132 ; Conservative 0 ; Mismatches 24 ; Indels 0 ; Gaps 0 ;

Qy      44  tctctcaacctccgataataacagagggatcccccgcgcgcatactgagcctccgctc 103
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Db      1  TCTGCTTCTCTCCGGAGAAATAACAGCGCTTCGCCGCCGCGCATGAGGCTCCCGGCGG 60

Qy      104  tctcagacgagccctctctctccgcgcgccttctcctcagtgatgtttcttgcgcgccttgatt 163
        |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      61  CCGGAGATGTCCTTTCCTTCCTCGGCGCCTTTCCTGAGTCTGAGTCTTCGCGGCATGATGTT 120

Qy      164  gctgctgtctcctctctccgatacaatgcaatgtcc 199
        |||||  |||||  |||||  |||  |||  |||
Db      121  GCTGCTGTACTCCTTCTCCGATGCTGTGAGAGGCC 156

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RESULT 1-  
 US-08-482-148-8  
 Sequence 8, Application US/08482148  
 Patent No. 5847082  
 GENERAL INFORMATION:  
 APPLICANT: Roether, Russell  
 APPLICANT: . Rollins, Scott  
 APPLICANT: Squitro, Stephen P  
 TITLE OF INVENTION: Terminal Complement  
 TITLE OF INVENTION: Inhibitor fusion Genes and Proteins  
 NUMBER OF SEQUENCES: 17  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Seth A. Fidel  
 STREET: Alexion Pharmaceuticals, 25 Science Park  
 CITY: New Haven  
 STATE: Connecticut  
 COUNTRY: USA  
 ZIP: 06511  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.4 Mb storage  
 COMPUTER: IBM compatible (pentium)  
 OPERATING SYSTEM: Windows 95 under MS DOS  
 SOFTWARE: Microsoft word for Windows  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/482,148  
 FILING DATE: 6/07/95  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fidel, Seth A.  
 REGISTRATION NUMBER: 38,449  
 REFERENCE/DOCKET NUMBER: ALX-129.1 Div  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (203) 776 1790  
 TELEFAX: (203) 772 3655  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1530 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Double  
 TOPOLOGY: Linear  
 MOLECULE TYPE: cDNA to mRNA  
 DESCRIPTION: MCP (CD46) full length cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 PUBLICATION INFORMATION:  
 AUTHORS: Lublin, D.M.  
 AUTHORS: Liszewski, M.K.  
 AUTHORS: Post, T.W.  
 AUTHORS: Arce, M.A.  
 AUTHORS: Lebeau, M.M.  
 AUTHORS: Rebentisch, M.B.

AUTHORS: Lemons, R.S.  
AUTHORS: Seya, T.  
AUTHORS: Atkinson, J.P.  
TITLE: Molecular cloning and Chromosomal  
TITLE: Localization of Membrane Cofactor  
TITLE: Protein (MCP): Evidence for Inclusion  
TITLE: In the Multi-Gene Family of  
TITLE: Complement-Regulatory Proteins.  
JOURNAL: Journal of Experimental Medicine  
VOLUME: 168  
PAGES: 181-194  
DATE: 1988  
US-08-482-148-8

Query Match 18.8%; Score 117.6; DB 2; Length 1530;  
Best Local Similarity 84.6%; Pred. No. 4.5e-28;  
Matches 132; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

44 tctgtcacctccgcgataatcaacgaggtctcccgccgcgtcatgagcctcccgctcg 103  
||||| ||||||| ||||| ||||| ||||||| ||||| ||||||| ||||| ||||| |||||  
Db 1 TCTGCTTCTCCTCCGAGAAATACAGCGCTCTCCGCGCGCATGAGAGCCTCCCGGCG 60  
QY 104 tctgagcgctcccttccctcccgcgcttccctggtgttcttctgagcgccctggtgtt 163  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||  
Db 61 CCGCAGAGTGCTCCTTCTCTCGCGCTTCTCTGCGCTTCTGCGCGCATGAGTGT 120  
QY 164 gctgtgtctctctctccgcgataatgcaatgtccc 199  
||||| ||||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 GCTGCTGACTCTTCTCCGATGCTGTGAGAGACC 156

RESULT 12  
PCT-US95-02944-8

; Sequence 8, Application PC/TUS9502944

; GENERAL INFORMATION:  
; APPLICANT: Rother, Russell  
; APPLICANT: Rollins, Scott  
; APPLICANT: Squinto, Stephen P  
; TITLE OF INVENTION: Terminal Complement  
; TITLE OF INVENTION: Inhibitor Fusion Genes and Proteins  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Maurice M. Klee  
; STREET: 1951 Burr Street  
; CITY: Fairfield  
; STATE: Connecticut  
; COUNTRY: USA  
; ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 720 Kb storage

COMPUTER: Dell 486/50

OPERATING SYSTEM: DOS 6.2

SOFTWARE: Word Perfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02944

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/205,720

FILING DATE: 3-MAR-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Klee, Maurice M.

REGISTRATION NUMBER: 30,399

REFERENCE/DOCKET NUMBER: ALX-129PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 255 1400

TELEFAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1530 base pairs

TYPE: Nucleic Acid

STRANDEDNESS: Double  
TOPOLOGY: Linear  
MOLECULE TYPE: cDNA to mRNA  
DESCRIPTION: MCP (CD46) full length cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
PUBLICATION INFORMATION:  
AUTHORS: Lublin, D.M.  
AUTHORS: Liszewski, M.K.  
AUTHORS: Post, T.W.  
AUTHORS: Arce, M.A.  
AUTHORS: Lebeau, M.M.  
AUTHORS: Rebentisch, M.B.  
AUTHORS: Lemons, R.S.  
AUTHORS: Seya, T.  
AUTHORS: Atkinson, J.P.  
TITLE: Molecular cloning and Chromosomal  
TITLE: Localization of Membrane Cofactor  
TITLE: Protein (MCP): Evidence for  
TITLE: Inclusion in the Multi-Gene Family  
TITLE: of Complement-Regulatory Proteins.  
JOURNAL: Journal of Experimental Medicine  
VOLUME: 168  
PAGES: 181-194  
DATE: 1988  
PCT-US95-02944-8

Query Match 18.8%; Score 117.6; DB 5; Length 1530;  
Best Local Similarity 84.6%; Pred. No. 4.5e-28;  
Matches 132; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 44 tctgtcacctccgcgataatcaacgaggtctcccgccgcgtcatgagcctcccgctcg 103  
||||| ||||||| ||||| ||||| ||||||| ||||| ||||||| ||||| ||||| |||||  
Db 1 TCTGCTTCTCCTCCGAGAAATACAGCGCTCTCCGCGCGCATGAGAGCCTCCCGGCG 60  
QY 104 tctgagcgctcccttccctcccgcgcttccctggtgttcttctgagcgccctggtgtt 163  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||  
Db 61 CCGCAGAGTGCTCCTTCTCTCGCGCTTCTCTGCGCTTCTGCGCGCATGAGTGT 120  
QY 164 gctgtgtctctctccgcgataatgcaatgtccc 199  
||||| ||||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 GCTGCTGACTCTTCTCCGATGCTGTGAGAGACC 156

RESULT 13

PCT-US95-02945-3

; Sequence 3, Application PC/TUS9502945

; GENERAL INFORMATION:

; APPLICANT: Fodor, William L

; APPLICANT: Rollins, Scott

; APPLICANT: Squinto, Stephen P

; TITLE OF INVENTION: Chimera Complement

; TITLE OF INVENTION: Inhibitor Proteins

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Maurice M. Klee

; STREET: 1951 Burr Street

; CITY: Fairfield

; STATE: Connecticut

; COUNTRY: USA

; ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 750 Kb storage

COMPUTER: Dell 486/50

OPERATING SYSTEM: DOS 6.2

SOFTWARE: WordPerfect 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/02945

FILING DATE:

CLASSIFICATION:

```

PCT-EP08769-A1
PCT APPLICATION DATA :
APPLICATION NUMBER: 08/205,508
FILING DATE: 3-MAR-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-120PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-1400
TELEFAX: (203) 254-1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1530 bases
TYPE: Nucleic Acid
STRADEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: MCP (CD46) full length cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Lublin, D.M.
AUTHORS: Liszewski, M.K.
AUTHORS: Post, T.W.
AUTHORS: Arce, M.A.
AUTHORS: LeBeau, M.M.
AUTHORS: Rebentisch, M.B.
AUTHORS: Lemons, R.S.
AUTHORS: Seya, T.
AUTHORS: Atkinson, J.P.
TITLE: Molecular cloning and Chromosomal
TITLE: Localization of Membrane Cofactor
TITLE: Protein (MCP): Evidence for
TITLE: Inclusion in the Multi-Gene Family
TITLE: of Complement-Regulatory Proteins.
JOURNAL: Journal of Experimental Medicine
VOLUME: 168
PAGES: 181-194
DATE: 1988
PCT-US95-02945-3

Query Match      18.8%; Score 117.6; DB 5; Length 1530;
Best Local Similarity   84.6%; Pred.No.4.5e+28;
Matches 132; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

    44 tctgtcaactccgataaatcagggagtctccgcgcccgtcatcaggcgcttccgcgtccg
        | ||||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     1 ttctgttttcctccggaagaatracacgccgtttccgcgcgcattgagaccgtccccgccc 60

QY    104 tcctcagagctcccttcccttcccgagcgcttcccttgattgtctcttgagcgacctgatt 163
       | |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 ccgcgagtagtcccttcttcttcccttgctggcgctttccttgsgtgttgcggccatgstgtt 120

QY    164 gctcgtgtctcctctctctccgatgcataatgccaatgtccc 199
       ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     121 gcttctgtactcttcttccgatgcctgtgagagacc 156

RESULT_14
5514787-1
Patent No. 5514787
Applicant: ARKINSON, JOHN P.
Title of Invention: DNA SEQUENCES ENCODING HUMAN MEMBRANE
COFACTOR PROTEIN (MCP)
Number of Sequences: 2
Current Application Data:
Application Number: US/07/948,350
Filing Date: 21-SEP-1992
Prior Application Data:
```

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; APPLICATION NUMBER: 384,210
; FILING DATE: 21-JUL-1989
; SEQ ID NO:1
; LENGTH: 1546
5514787-1

Query Match      18.8%; Score 117.6; DB 6; Length 1546;
Best Local Similarity 84.6%; Pred.No. 4.5e-28;
Matches 132; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY      44  tctgtcaactcgcgataatacatcagggtctccgcgcgcctcatgagcctccgtccg 103
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB       1  tctgtcttctctcgcgagaataacagcgtcttccgcgcgcgcatgagcctccgcgcg 60
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY      104 tctcagagctcccttctcttccgcgcgtcttcttggtgtcttcttgagccctgtgtt 163
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB       61  ccgcgagttcccttcttcttccgtcgcgttcttggtgtcttcttgagccatgtgtt 120
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY      164 gctgtgtctctctcttccatcatgcatgtccc 199
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB       121 gctgtgtactctcttccatgcatgtgtgagagcc 156
         ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-08-435-149-17
; Sequence 17, Application US/08435149
; Patent No. 5866402
; GENERAL INFORMATION:
; APPLICANT: INNIS, MICHAEL A.
; APPLICANT: ZAROR, ISABEL
; APPLICANT: CREASEY, ABELA A.
; TITLE OF INVENTION: CHIMERIC MCP AND DAF PROTEINS WITH CELL
; TITLE OF INVENTION: SURFACE LOCALIZING DOMAIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
; CITY: EMERYVILLE
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,149
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVEREIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0989,001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-435-149-17

Query Match      18.6%; Score 116.6; DB 2; Length 1878;
Best Local Similarity 84.3%; Pred.No. 1.1e-27;
Matches 131; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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